



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 176413

TO: Rosanne Kosson
Location: REM/3B84/3C70
Art Unit: 1653
Friday, January 13, 2006
Case Serial Number: 10/615515

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Kosson,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:06:13 ; Search time 21 Seconds
(without alignments)
2464.982 Million cell updates/sec

Title: US-10-615-515-6
Perfect score: 2787
Sequence: 1 MESSVNOQPLNEKQIANSQ.....MCGFTGALDIVINFTLDMI 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2787	100.0	538	2	A31760 Ro/SS-A complex, 6
2	2269	81.4	538	2	ribonucleoprotein
3	1011	36.3	643	2	T19225 Ro autoantigen 60K
4	798.5	28.7	531	2	C75418 ribonucleoprotein
5	180.5	6.5	719	2	S55939 telomerase compone
6	130.5	4.7	1937	2	I38055 myosin heavy chain
7	125.5	4.5	1938	1	JX0178 myosin heavy chain
8	122	4.4	439	2	C64401 myosin heavy chain
9	119.5	4.3	876	2	A21767 myosin heavy chain
10	119	4.3	1938	2	A53293 skeletal myosin he
11	118.5	4.3	1157	2	T43259 pyruvate:ferredoxi
12	118	4.2	713	2	S70434 zona pellucida gly
13	118	4.2	836	2	T42323 hypochetical prote
14	117.5	4.2	741	2	S39082 myosin heavy chain
15	117.5	4.2	955	2	S24348 myosin heavy chain
16	116.5	4.2	373	2	G75073 hypochetical prote
17	116	4.2	394	2	T45875 hypochetical prote
18	116	4.2	1024	2	H86331 hypochetical prote
19	115.5	4.1	571	2	H82268 arginine decarboxy
20	115	4.1	615	2	F64572 myosin heavy chain
21	114.5	4.1	1128	2	G86266 hypochetical prote
22	114.5	4.1	1175	2	T46124 hypochetical prote
23	114.5	4.1	1418	2	S64918 hypochetical prote
24	114	4.1	1351	2	B97273 superfamily I DNA
25	113.5	4.1	1496	2	T05634 hypochetical prote
26	113.5	4.1	2025	2	JC5020 tetraeticopeptide
27	113	4.1	1577	2	T19722 hypochetical prote
28	112.5	4.0	936	2	S39083 myosin heavy chain
29	111.5	4.0	698	2	S52696 myosin heavy chain

30	111.5	4.0	1606	2	T34073 paramerin - chicke
31	111	4.0	1940	2	A29320 myosin heavy chain
32	110.5	4.0	1157	2	T43258 pyruvate:ferredoxi
33	110.5	4.0	2094	2	S33124 tpr protein - huma
34	110	3.9	15281	2	S41309 cyclosporin synthe
35	109.5	3.9	1948	2	S00485 gene 11-1 protein
36	109	3.9	478	2	D30169 leukotoxin secreti
37	108.5	3.9	1179	2	P71190 probable chromoso
38	107.5	3.9	1039	2	S61819 myosin heavy chain
39	107.5	3.9	1085	2	F96712 hypochetical prote
40	107	3.8	533	2	T36919 hypochetical prote
41	106.5	3.8	1940	1	A24922 myosin heavy chain
42	106	3.8	394	2	B89780 ornithine aminotra
43	106	3.8	703	2	T48559 probable receptor-
44	106	3.8	1033	2	A96714 hypochetical prote
45	105.5	3.8	420	2	S55272 DNA-binding protei

ALIGNMENTS

RESULT 1

A31760
Ro/SS-A complex, 60K ribonucleoprotein - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: A31760; A30596
R:Deutscher, S.L.; Harley, J.B.; Keene, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 9479-9483, 1988
A:Title: Molecular analysis of the 60-kDa human Ro ribonucleoprotein.
A:Reference number: A31760; MUID:89071722; PMID:3200833

A:Accession: A31760
A:Molecule type: mRNA
A:Residues: 1-538 <DED>
A:Cross-references: UNIPROT:P10155; UNIPARC:UPI00004EEBA; GB:J04137; NID:g177782; PIDN:f
R:Ben-Chetrit, E.; Gandy, B.J.; Tan, R.M.; Sullivan, K.F.
J. Clin. Invest. 83, 1284-1292, 1989
A:Title: Isolation and characterization of a cDNA clone encoding the 60-kD component of t
A:Reference number: A30596; MUID:89198084; PMID:2649513
A:Accession: A30596
A:Molecule type: mRNA
A:Residues: 1-238, 'R', 240-292, 'DV', 295-300, 'A', 302-514, 'ALONTLANKSF' <BEN>
A:Cross-references: UNIPARC:UPI0000179666; GB:M25077; NID:g387656
A:Note: The sequence is revised in Genbank entry HUMANTRANP, release 111.0, (PID:g387657)
C:Genetics:
A:Gene: GDB:SSA2
A:Cross-references: GDB:355563; OMIM:600063
A:Map position: 1q31-1q31
C:Keywords: DNA binding; zinc finger
F:305-323/Region: zinc finger CCH motif

Query Match 100.0%; Score 2787; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-181;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESSVNOQPLNEKQIANSQSGYVQVYDANRLHFLPGSGSGGYVYKQQLGLENEA	60
DB	1	MESSVNOQPLNEKQIANSQDGYVQVYDMMNLHFLPGSGSGGYVYKQQLGLENEA	60
QY	61	LIRLIEDRGCEVIOEIKSFSGEGRTRKOEPMFLALAIQSGSDISTKQAFKAVSEVCR	120
DB	61	LIRLIEDRGCEVIOEIKSFSGEGRTRKOEPMFLALAIQSGSDISTKQAFKAVSEVCR	120
QY	121	IFTHLFTFIQFKDDKESMKCGMGRALRKALADWYNEKGMALALAVTKYQRNGWSHK	180
DB	121	IFTHLFTFIQFKDDKESMKCGMGRALRKALADWYNEKGMALALAVTKYQRNGWSHK	180
QY	181	DILRLSHLKPSSEGLAIVTKYITTKGKVEHETKXKALSVETBEKLKYLEAVEKVRTD	240
DB	181	DILRLSHLKPSSEGLAIVTKYITTKGKVEHETKXKALSVETBEKLKYLEAVEKVRTD	240
QY	241	ELEVHLTEHRVLVEHLLTNLKSKEVKKALLOEMPLTALLRNIGKMTANSVLEPGENSE	300
DB	241	ELEVHLTEHRVLVEHLLTNLKSKEVKKALLOEMPLTALLRNIGKMTANSVLEPGENSE	300

Db 241 ELEVIHILIEBHRLVREHLTNHLKSKVEWKALLQEMPLTALLRLNLGKMTANSVLEPGNSE 300

Qy 301 VSLVCEGLCNEKLLKKARIPPHILLALETYKTHGIRGLKLRPRDEIILKALDAAYKT 360

Db 301 VSLVCEGLCNEKLLKKARIPPHILLALETYKTHGIRGLKLRPRDEIILKALDAAYKT 360

Qy 361 FKTYEPFGKFFLADVSAŠNNORVLGŠIINASTVAAMCMVVTTRTEKDSVYVAFSDENV 420

Db 361 FKTYEPFGKFFLADVSAŠNNORVLGŠIINASTVAAMCMVVTTRTEKDSVYVAFSDENV 420

Qy 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPTADVIFVFTDNTEPAGVHPA 480

Db 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPTADVIFVFTDNTEPAGVHPA 480

Qy 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDNGCFDGLADVIRNFTLDMI 538

Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDNGCFDGLADVIRNFTLDMI 538

RESULT 2

151560 ribonucleoprotein - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: 151560

R/O'Brien, C.A.; Margelot, K.; Molin, S.L.

Proc. Natl. Acad. Sci. U.S.A. 90, 7250-7254, 1993

A/Title: Xenopus Ro ribonucleoprotein: members of an evolutionarily conserved class of

A/Reference number: A48294; MUID:93348251; PMID:7688474

A/Accession: 151560

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-538 <OAB>

A/References: UNIPROT:P42700; UNIPARC:UPI000013450E; GB:L15430; NID:g295535; PIDN:

Query Match 81.4%; Score 2269; DB 2; Length 538;

Best Local Similarity 78.6%; Pred. No. 2.4e-146;

Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;

Qy 1 MEESVNOQPLNEKQIANSODGYVQVTDNRHLRFLCFSGEGGTYIIEKQGLGENAE 60

Db 1 MEATMDQTOPLNKQVNSBECYVQVSDMKRLRFLCFSGEGGTYIIEKQGLGENAE 60

Qy 61 LIRLIEGRGCEVQEIETKSPQSEGRITKQBPMLFALICSGCSNISTKQAFKAVSVCR 120

Db 61 LIRLIEGRGCEVQEIETKSPQSEGRITKQBPMLFALICSGCSNISTKQAFKAVSVCR 120

Qy 121 IPTHLPFIQPKDKLKSMMCGMGRALRKALADWYNEKGMLALAVTKYKORNGWSHK 180

Db 121 IPTHLPFIQPKDKLKSMMCGMGRALRKAVSDWYNTKQALNLAAMVTKYKORNGWSHK 180

Qy 181 DLRLSLHAKSSBGLAVTKYITKGMKEVHELYEKLAVTEGLKYLLEAVEKYKTKD 240

Db 181 DLRLSLHAKSSBGLAVTKYITKGMKEVHELYEKLAVTEGLKYLLEAVEKYKTKD 240

Qy 241 ELLEVIHILIEBHRLVREHLTNHLKSKVEWKALLQEMPLTALLRLNLGKMTANSVLEPGNSE 300

Db 241 ELLEVIHILIEBHRLVREHLTNHLKSKVEWKALLQEMPLTALLRLNLGKMTANSVLEPGNSE 300

Qy 301 VSLVCEGLCNEKLLKKARIPPHILLALETYKTHGIRGLKLRPRDEIILKALDAAYKT 360

Db 301 VSLVCEGLCNEKLLKKARIPPHILLALETYKTHGIRGLKLRPRDEIILKALDAAYKT 360

Qy 361 FKTYEPFGKFFLADVSAŠNNORVLGŠIINASTVAAMCMVVTTRTEKDSVYVAFSDENV 420

Db 361 FKTYEPFGKFFLADVSAŠNNORVLGŠIINASTVAAMCMVVTTRTEKDSVYVAFSDENV 420

Qy 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPTADVIFVFTDNTEPAGVHPA 480

Db 421 PCPVTDMTLOQVLMANSQIPAGGTDCLPMVMAQKNTPTADVIFVFTDNTEPAGVHPA 480

Qy 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDNGCFDGLADVIRNFTLDMI 538

Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDNGCFDGLADVIRNFTLDMI 538

Db 481 TALQYREKMGIPAKLIVCGMTSNGFSIADPDDRGMLDICGDSGALDVIRNFTLDMI 538

RESULT 3

T19225

Ro autoantigen 60k homolog - Caenorhabditis elegans

N/Alternate names: Ropip protein

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T19225; J04574; T26556

R/McMurray, A.

Submitted to the EMBL Data Library, June 1996

A/Reference number: Z19092

A/Accession: T19225

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-643 <ML>

A/Cross-references: UNIPROT:Q27274; UNIPARC:UPI000013450C; EMBL:Z73969; PIDN:CAA98241.1;

A/Experimental source: clone C12D8

R/Labbe, J.C.; Jannatipour, M.; Rokeach, L.A.

Gene 167, 227-231, 1995

A/Title: The Caenorhabditis elegans rop-1 gene encodes the homologue of the human 60-kDa

A/Reference number: J04574; MUID:96144279; PMID:8566782

A/Accession: J04574

A/Molecule type: mRNA

A/Residues: 1-643 <LAB>

A/Cross-references: UNIPARC:UPI000013450C; GB:U21487; NID:g905358; PIDN:AAA96949.1; PID:

R/Gardner, A.

Submitted to the EMBL Data Library, January 1998

A/Reference number: Z20231

A/Accession: T26556

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-643 <M12>

A/Cross-references: UNIPARC:UPI000013450C; EMBL:AL021479; PIDN:CAA16325.1; GSPDB:GN00023;

A/Experimental source: clone Y22F5A

C/Comment: This protein is a main protein constituent associated with the RNA in the Ro

C/Genetics:

A/Gene: rop-1

A/Map position: 5; V

A/Introns: 24/2; 272/3; 329/2; 545/3

F/139-333/Domain: RNA binding #statue predicted <RNB>

F/140-145/Region: ribonucleoprotein similarity

F/189-197/Region: ribonucleoprotein similarity

F/291-295/Region: nuclear location signal

F/419-422/Region: nuclear location signal

F/588-591/Region: nuclear location signal

Query Match 36.3%; Score 1011; DB 2; Length 643;

Best Local Similarity 36.3%; Pred. No. 7.8e-61;

Matches 215; Conservative 111; Mismatches 204; Indels 62; Gaps 9;

Qy 7 QMPLNEKQIANSODGYVQVTDNRHLRFLCFSGEGGTYIIEKQGLGENAEALYILIE 66

Db 54 QMEKVDQGVENNAAGVFPEVSDQVRRFLIGSPKGSYHOSSEKITTINDAORIIKIE 113

Qy 67 DGRGCEVIGIKSPQSEGRITKQBPMLFALICSGCSNISTKQ----- 109

Db 114 QGSHVHLKALILINBNRPKNAMIFTLAICARISTHDITKTBCEPMLANYSDIYAL 173

Qy 110 --AFAVSEVCRIPHLFTFIQPKDKLKSMMCG-----MMGRALRKALADWYNEKG 161

Db 174 HDSALDLIPVCRTPHLFPFVYCGTISSTYAGGAKSSTGGRSBRNAISKYYTKTT 233

Qy 162 MALALAVTKYKORNGWSHDKLRLSH--LKPSSEGLA-----IVTKYITG----- 205

Db 234 EKLAMLTCKYQREBSHRDLFRLAHPNLMDSSHGSEDLRLREBQLFRPAVVGDLVXRK 293

Qy 206 -----KGVNHLIYEKALSV-----ETBKLLKYLEAVKRYKTKDELEVHILI 248

Db 294 RKNVSVEVAEVEVSWCKAKLPYTBEOQLIKEQSRALNIVEYLLKLNQSESEVIAAI 353

Qy 249 EBRRLVREHLTNHLKSKVEWKALLQ-EMPLTALLRLNLGKMTANSVLEPGNSEVSLVCEK 307

Db 354 KKGIGLVNHEPPTSSINSKLVWETLFDVSNMTMIRRLAQTVVGAJD--EKGVNDIVKR 411
Qy 308 LCNEKLLKQARIHFFHLLIALETYKTHGIRGKLKMPDDEILKALDAAFYKPKYVEPT 367
Db 412 LTPDEELRRRIHRIINLLTAAVVAQGRBGDGSFTMEPNCQICDALSAGYKAFVNAAPT 471
Qy 368 GKRELLAVDVASASNOEVLGSLINASTVAAACMVVTRTEKDSYVAFSDENVPCTYTD 427
Db 472 GKRCYCALDVSGSMTSRVSSPISCREAAGMSILINHNELAVACVAFCKLTELPEPTKO 531
Qy 428 MTLQOYVLAASQIPAGGTCSLPMIWAQKTTTPADVEIVFTDNETPAGVHPALALREYR 487
Db 532 WKIGQVNDVYNNNDLFGRTDGLPMTWATENNLLKPDVFIIYTDNDTWAGEIHPFAIKCYR 591
Qy 488 KQANDI-PAKLIYCGMSTNGPTIADPDRGMIDMGSGPDGALDYVRNNTLDMI 538
Db 592 EASGIHDAKVLVMMQAVDYSIADPSSDKMILDTGFSAFVAFQIYHEBVTGKI 643

[illegible]

RESULT 6

138055 myosin heavy chain, perinatal skeletal muscle - human
 N/Contains: myosin ATPase (EC 3.6.4.1)
 C/Species: Homo sapiens (man)
 C/Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
 C/Accession: J38055; JH0154; S12459; S09332; A30220; S49478
 R/Jullian, E.H.; Kelly, A.M.; Pomidou, A.J.; Hoffman, R.; Schiaffino, S.; Steadman, H.H.
 Eur. J. Biochem. 230, 1001-1006, 1995
 A/Title: Characterization of a human perinatal myosin heavy-chain transcript.
 A/Reference number: J38055; MUID:95324556; PMID:7601129
 A/Accession: J38055
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1937 <RES>
 A/Cross-references: UNIPROT:P13535; UNIPARC:UPI000016ADAD9; EMBL:Z38133; NID:9558668; PIR
 R/Karsch-Mizrachi, I.; Feghali, R.; Shows, T.B.; Leinwand, L.A.
 Gene 89, 289-294, 1990
 A/Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.
 A/Reference number: JH0154; MUID:90323631; PMID:2373371
 A/Accession: JH0154
 A/Molecule type: mRNA
 A/Residues: 1-14, 'A', 16-859 <KAR>
 A/Cross-references: UNIPARC:UPI000017760F; GB:Y00821
 A/Experimental source: skeletal muscle
 R/Bober, E.
 Submitted to the EMBL Data Library, January 1989
 A/Reference number: S12458
 A/Accession: S12459
 A/Molecule type: mRNA
 A/Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>
 A/Cross-references: UNIPARC:UPI000016A5F8; EMBL:X51592; NID:929465; PIDN:CAJ35941.1; PIR
 A/Experimental source: clone gEMC-F
 R/Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
 Eur. J. Biochem. 189, 55-65, 1990
 A/Title: Identification of three developmentally controlled isoforms of human myosin hea
 A/Reference number: S09331; MUID:90235862; PMID:1691980
 A/Accession: S09332
 A/Molecule type: mRNA
 A/Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 899-
 -1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668-17
 A/Cross-references: UNIPARC:UPI0000177610; EMBL:X51592
 R/Feghali, R.; Leinwand, L.A.
 J. Cell Biol. 108, 1791-1797, 1989
 A/Title: Molecular genetic characterization of a developmentally regulated human perinat
 A/Reference number: A30220; MUID:89234168; PMID:2715179
 A/Accession: A30220
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-184
 A/Cross-references: UNIPARC:UPI0000177611; GB:Y00821; NID:934863; PIDN:CAJ68757.1; PID:9
 C/Genetics:
 A/Gene: GDB:MYH8
 A/Cross-references: GDB:125267; OMIM:160741
 A/Map position: 17pter-17p12
 C/Superfamily: myosin heavy chain; myosin motor domain homology
 C/Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
 F/91-769/Domain: myosin motor domain homology <MOTOR>
 F/181-188/Region: nucleotide-binding motif A (P-loop)
 F/551-588/Region: actin binding #status predicted
 F/658-680/Region: actin binding #status predicted
 F/842-1282/Region: S2 #status predicted
 F/938, 708/Active site: Cys #status predicted
 Query Match 4.7%; Score 130.5; DB 2; Length 1937;
 Best Local Similarity 20.0%; Pred. NO. 2.1;
 Matches 101; Conservative 72; Mismatches 168; Indels 165; Gaps 18;

Db 1315 IEEIKQLEBEETAKVAAALAAALQSSRHDCDLTREOYEEDEGKAEIQ----- 1361
 Qy 103 SDISTKQAPKAVSEVCRIPTHLFT-FIQKKDLK-----SMKCG 142
 Db 1362 -----RLSKANSSEVAQMTKTKETDALIQTELEEKKKLQAQRLDAEEHVEAVNAKCA 1415
 Qy 143 MNGRALRKAIADVYNEKGMAL-----ALATYKKQRN-----GMSHK----- 180
 Db 1416 ----SLEKTKQRQNEVEDLMDVERSNMAACALDKQRNFDKVLSEMKQKVEETQALE 1471
 Qy 181 -----DLRLSHL-----KPSSEGLAVTKYTKGKVEHELYK 214
 Db 1472 ASQKESRLSTELFKVKNVVEESLDQLETLRRENKMLQGEISDLTEQIAEGCKQIHLEK 1531
 Qy 215 EKSLSTETELKYLDAVEKVKTKDELYTHLIEHRVLRHLLTHLSKSEVWKALQ 274
 Db 1532 IKK-QVEQK-----EIQALEAEASLEHEGKILRIQLELNQVXSVDRTAK 1582
 Qy 275 EMPFLTLRLGLGM--TANSLBPG-----NSEVSLVCEK 307
 Db 1583 DEEIDQLKRNHTVETWQSTLDABIRSDALRYKKKEGDLNEMEIQLNHNRLAAES 1642
 Qy 308 LCN-----EKLKKARLHPHILLALETYKTGHLRGKLRKRPDEILK---ALDAAFYK 359
 Db 1643 LRNVYNTQGITKETQLH-----LDALRGQEDLEKQLAIVERBANLLQAEIEE 1690
 Qy 360 TFKTVPTGKRFLLAVDVASNNQRY 385
 Db 1691 LWTATLEOTERSRKIAQBELLDASERV 1716

RESULT 7

JX0178 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken
 N/Contains: myosin ATPase (EC 3.6.4.1)
 C/Species: Gallus gallus (chicken)
 C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 31-Dec-2004
 C/Accession: PX0050; PX0051; JX0178; A26365; S02082; PM0009; S39081; S24351; S05;
 R/Hayashida, M.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 54-59, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the
 A/Reference number: PX0050; MUID:92041767; PMID:1939027
 A/Accession: PX0050
 A/Molecule type: protein
 A/Residues: 1-205 <HAY>
 A/Cross-references: UNIPROT:Q90913; UNIPROT:Q90909; UNIPARC:UPI0000173E18
 R/Komine, Y.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 60-67, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of the
 A/Reference number: PX0051; MUID:92041768; PMID:1939028
 A/Accession: PX0051
 A/Molecule type: protein
 A/Residues: 206-636 <KOM>
 A/Cross-references: UNIPARC:UPI0000173E19
 R/Maita, T.; Miyaniishi, T.; Matsuzono, K.; Tanloka, Y.; Matsuda, G.
 J. Biochem. 110, 68-74, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of t
 A/Reference number: PX0052; MUID:92041769; PMID:1939029
 A/Accession: PX0052
 A/Molecule type: protein
 A/Residues: 201-213;632-837 <MAI>
 A/Cross-references: UNIPARC:UPI0000173E1A; UNIPARC:UPI0000173E1B
 R/Maita, T.; Yajima, E.; Negata, S.; Miyaniishi, T.; Nakayama, S.; Matsuda, G.
 J. Biochem. 110, 75-87, 1991
 A/Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of the
 A/Reference number: JX0178; MUID:92041770; PMID:1939030
 A/Accession: JX0178
 A/Molecule type: protein
 A/Residues: 833-1938 <MA2>
 A/Cross-references: UNIPARC:UPI0000173E1C
 R/Maita, T.; Hayashida, M.; Tanloka, Y.; Komine, Y.; Matsuda, G.
 Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987

A/Title: The primary structure of the myosin head.
A/Reference number: A26365; MUID:87092420; PMID:3647365
A/Accession: A26365
A/Molecule type: protein
A/Residues: 1-129, 'X', 131-139, 141-550, 'X', 552-754, 'X', 756-784, 'Q', 787-804, 806-810 <MA3>
A/Cross-references: UNIPARC:UPI0000173E1D
R/Matanabe, B.
Biol. Chem. Hoppe-Seyler 370, 55-61, 1989
A/Title: Amino-acid sequence of the hinge region in chicken myosin subfragment-2.
A/Reference number: 802082; MUID:89228549; PMID:2713098
A/Accession: 802082
A/Molecule type: protein
A/Residues: 1144-1270 <MAT>
A/Cross-references: UNIPARC:UPI0000173E1E
R/Yajima, E.
Nagasaki Igakka! Zasshi 65, 409-430, 1990
A/Title: Study on tail region of skeletal muscle myosin; primary structure and protease
A/Reference number: PM0009
A/Accession: PM0009
A/Molecule type: protein
A/Residues: 1304-1938 <YAJ>
A/Cross-references: UNIPARC:UPI0000173E1F
R/Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
Submitted to the EMBL Data Library, August 1991
A/Description: Analysis of the chicken fast myosin heavy chain family: Localization of
A/Reference number: S39081
A/Accession: S39081
A/Molecule type: mRNA
A/Residues: 1081-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1795, 'HV', 1798-1829, 'S', 1831
A/Cross-references: UNIPARC:UPI0000173E20; EMBL:M74084
R/Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A/Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
A/Reference number: 824351; MUID:92309413; PMID:1377278
A/Accession: 824351
A/Molecule type: mRNA
A/Residues: 1082-1182, 'T', 1184-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1780, 'W', 1782-
A/Cross-references: UNIPARC:UPI0000173E21; EMBL:M74084
R/Matanabe, B.
Biol. Chem. Hoppe-Seyler 370, 1027-1034, 1989
A/Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal muscle
A/Reference number: 805515; MUID:90121764; PMID:2610940
A/Accession: 805515
A/Molecule type: protein
A/Residues: 842-906, 'Q', 908-1270 <MA3>
A/Cross-references: UNIPARC:UPI0000173E22
R/Matanabe, B.
Biol. Chem. Hoppe-Seyler 370, 549-558, 1989
A/Title: Amino-acid sequence of the short subfragment-2 in adult chicken skeletal muscle
A/Reference number: 804501; MUID:89374803; PMID:2775482
A/Accession: 804501
A/Molecule type: protein
A/Residues: 852-906, 'Q', 908-1108 <MA2>
A/Cross-references: UNIPARC:UPI0000173E23
R/Matsuda, G.; Maita, T.; Miyashita, T.; Hayashida, M.
J. Protein Chem. 6, 33-46, 1987
A/Title: Structure and function of muscle myosin.
A/Reference number: A60877
A/Accession: A60877
A/Molecule type: protein
A/Residues: 1-139, 141-205 <MA1>
A/Cross-references: UNIPARC:UPI0000173E24
R/Gulick, J.; Kropp, K.; Robbins, J.
J. Biol. Chem. 260, 14513-14520, 1985
A/Title: The structure of two fast-white myosin heavy chain promoters. A comparative stu
A/Reference number: A25207; MUID:86033956; PMID:2997212
A/Accession: A25207
A/Molecule type: DNA
A/Residues: 'M', 1-168 <GUL>
A/Cross-references: UNIPARC:UPI00000FB638; GB:M13512; GB:M12083; GB:M13510; NID:g212363;
R/Kropp, K.; Gulick, J.; Robbins, J.
J. Biol. Chem. 261, 6613-6618, 1986
A/Title: A canonical sequence organization at the 5'-end of the myosin heavy chain genes

A/Reference number: A92587; MUID:86196091; PMID:3009465
A/Accession: C25217
A/Molecule type: DNA
A/Residues: 'M', 1-56, 'T', 58-76, 'T', 78-168 <KRO>
A/Cross-references: UNIPARC:UPI00000PB4C9; GB:M13515; GB:M13511; NID:g212373; PIDN:AAA46;
C/Comment: This is a fragment of the globular head.
C/Superfamily: myosin motor domain homology
C/Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methylated
F/1-1938/Product: myosin heavy chain #status experimental <MAT>
F/89-768/Domain: myosin motor domain homology <MAT>
F/179-186/Region: nucleotide-binding motif A (P-loop)
F/550-587/Region: actin binding #status predicted
F/657-679/Region: actin binding #status predicted
F/841-1938/Domain: coiled coil <COI>
F/841-1289/Region: S2
F/852-1108/Domain: short subfragment 2 <SUB2>
F/1290-1938/Region: light meromyosin
F/1/Modified site: acetylated amino end (Ala) #status experimental
F/35/Modified site: N6-methyllysine (Lys) #status experimental
F/130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F/185/Binding site: ATP (Lys) #status predicted
F/697,707/Active site: Cys #status predicted
F/755/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 4.5%; Score 125.5; DB 1; Length 1938;
Best Local Similarity 20.0%; Pred. No. 4.6;
Matches 110; Conservative 82; Mismatches 208; Indels 149; Gaps 21;

2 EESVQMOPLNEK--QIANSQGYWQVTDNMRHLRFLCGSEGGTYIKKQKGLN-- 57
1266 EQNQRMINDTQGAIRLOTGERESRQAEKBDALISQSRKQGPQTQIEBKHLREBI 1325
58 --AARLRLIEDGR-GCEVIOEIKSPQEGRTTQBPMLFALICSCQSDISTQAAKA 114
1326 KAKNALNALQSAHDCDLLEQVEEBOEAKGELQ-----RALSKA 1366
115 VSEVCRIPTHLFT--FIQPKDLKESMK----- 140
1367 NSEVAQWRKYETALIQTELEBKKAQRLQDAEENVAANAKSLKTKORLQNE 1426
141 -----CGMWGRALR--KAIDW-----YNE-----KGMALAAVTKYKQ 173
1427 VEDLMVDERNSNAQALDKQKNPKDLKAWKQKYESTQTELEASQKESSTLSTFLKM 1486
174 RNSGSHKDLRLSH-----KPSBGLAVTYYTKGKVEHLYEYKALSVETECIL 226
1487 KNAVEES---LDHLLETAKRENKMLQOEIADLTQIAGGKAVHELEKVKR--HVEQEK-- 1539
227 KYLAEVKEVKTKQDELVIYHILIEHRVLREHLTNHKSKEVWKALLQEMPLTALRLYL 286
1540 -----SELQALAEBAEASLHEBEGKITRLQLELNQIKSEIDRKIAEKOBEIDQLKRNHL 1593
287 KM-----TANSVLEPGNSVSLVCEKLCNEKLKKAKIHPFH--LIALETKYGHGIRG 339
1594 RIVESMOSTLDAEIRSRKEARL---KKQEGDLNEMEIQLSHANRMAAABQKNLRNTQG 1650
340 KLK-----WRPDEI-----LKALDAFTKRTYVEPTGKRFLLAVDVAS 380
1651 TLKQTLHLDALRQEDLKEQVAMVERANMLQLEVELELGALEQTERSRKRAVEOEHL 1710
381 MNQRTGSIILNASTYAAAMCMVVTREDSYVVAFSDSMVCPTTMDTLQOVLMAMSOI 440
1711 ATERV--QLAHTQNTS---LINTKQKLETIDVQIQSEW-----EDTIQBARAEKA 1757
441 PAGGTDCSL 449
1758 KKAITDAAM 1766

RESULT 8
C64401
hypothetical protein MJ0811 - Methanococcus jannaschii
C/Species: Methanococcus jannaschii


```

Db      366 YEEBOEAKBEO-----RALSKANSEVAQWRTKKTETDAIQTEBELE 406
Qy      137 ESMK-----CGMGRALR 149
Db      407 EAKKGLQRLQDABEHVAEVAKACASLEKTKQRLQNEVEDLMDIVERANAACARLDKKQK 466
Qy      150 ---KAIADW---YNEKGG-----MALALAVTKKQKNGSHDRLRLSHL-----K 189
Db      467 NFDKILAEWKOKYEETQAELEASQKESRSLSSTELFKMKNAYEES---LDHLETLKRENK 522
Qy      190 PSSEGLAIVTKYITKGWKEVHELKYEKALSVETEKLLKYLEAVEKVKRTKDELFEVILHLE 249
Db      523 NLQOEISDLTEQIAEGGKAIHELEKVKK-QIEQEK-----SEIQALAEBAEASLEHE 573
Qy      250 EHLVREHLTNHLKSKEVWRFALLQEMPLTALRLNLRGM-----TANSVLEPGNSEVSL 303
Db      574 EGKILRLQLELNOVKSEIDRKIAEKDEBIDQKRNHLRIVESMSTLDABIRSRREALRL 633
Qy      304 VCEKLCNEKLLKARLHPFH-LIALETTYKTGHGLRGKJK-----WRPDEI----- 349
Db      634 ---KKMGEDLNEHEIQLNHANRVAAEAQXILRNTQGVLRKDTQIHLDDALRTQSDLEKQV 690
Qy      350 -----LKALDAFYKTFKTEVPTGKRPLAVDVASASNORVLSIINASTVAAAMCMNV 403
Db      691 AMVERRANLQAEIETELPALEQTERSRKRVABQELMDASERV--QLHTONTN---LIN 744
Qy      404 TRTEKDSYVVAFSDENVPCPYTTDWTLOOVLAMASQIPAGGIDCSL 449
Db      745 TKKULFTDIAQIQSEM-----EDTIQBARNAEBEKAKKAITDAM 783

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Search completed: January 13, 2006, 11:11:13
 Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:05:17 ; Search time 79 Seconds
(without alignments)
2992.225 Million cell updates/sec

Title: US-10-615-515-6
Perfect score: 2787
Sequence: 1 MEESVNMQNPINERQIANSO.....MCGPDGALDIVIRNFTLDMT 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003s:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2787	100.0	538	5	ABG32657 Human adh
2	2787	100.0	538	8	ADR99190 Sjogren s
3	2787	100.0	552	4	AA846827 Human ant
4	2782	99.8	553	4	AA846829 Human ant
5	2782	99.8	553	4	AA846828 Human ant
6	2659	95.4	525	8	AD841766 Protein B
7	2659	95.4	525	8	AD514359 Human SS-
8	1778	63.8	413	2	AAW03717 Human aut
9	1768	63.4	557	4	AA894864 Human pro
10	367	13.2	70	2	AA722511 Human RoR
11	185.5	6.7	641	4	AB859719 Drosophila
12	180.5	6.5	719	2	AA896038 80 kd pro
13	143.5	5.1	712	8	AD066766 Novel hum
14	143.5	5.1	1094	7	AD066766 Novel hum
15	130.5	4.7	1937	8	AD017289 Human sof
16	130.5	4.7	1937	8	AD017242 Human sof
17	130.5	4.4	3616	8	AD017242 Chicken A
18	130.5	4.3	824	7	AD017242 Human pro
19	130.5	4.3	892	7	AD017242 Human pro
20	130.5	4.3	892	7	AD017242 Human pro
21	130.5	4.3	892	7	AD017242 Human pro
22	119.5	4.3	876	8	AD017244 Human sof
23	118	4.2	876	8	AA851194 Porcine z
24	118	4.2	713	2	AAW81804 Porcine z

25	118	4.2	713	2	AA42467 Porcine z
26	118	4.2	713	3	AA52971 Porcine z
27	118	4.2	713	3	AA52971 Porcine z
28	118	4.2	713	3	AA52971 Porcine z
29	118	4.2	713	3	AA52971 Porcine z
30	117	4.2	23	2	AA43447 Ro/SSA ep
31	116	4.2	22	2	AA43447 Ro/SSA ep
32	115.5	4.1	550	7	AD865341 Human pro
33	115.5	4.1	571	6	ABU49243 Protein e
34	115.5	4.1	853	5	AB893794 Herbicide
35	115.5	4.1	1104	8	AD018225 Mouse GOB
36	115	4.1	561	2	AAW98552 H. pylori
37	115	4.1	1941	8	AD834528 POSH prot
38	114.5	4.1	1418	6	AB853853 Protein s
39	114.5	4.1	1418	7	ADK64930 Disease t
40	114.5	4.1	1418	8	ADK64930 Disease t
41	113.5	4.1	1715	5	AA022600 Tetraetic
42	113.5	4.1	1715	8	AD834529 POSH prot
43	113.5	4.1	1792	8	AD834530 POSH prot
44	113.5	4.1	2000	8	ADN04337 Antipsoi
45	113.5	4.1	2000	8	ADP24116 PRO polyp

ALIGNMENTS

RESULT 1
ABG32657 standard; protein; 538 AA.

XX ABG32657;

DT 15-NOV-2002 (first entry)

XX Human adhesion molecule, termed P10155 (Ro60 or AD55), protein.

XX Human; adhesion molecule; AD51; AD55; AAC74854.1; Ro60; AAC76768.1; P10155; embryogenesis; apoptosis; homeostasis; phenotypic; ligand; diagnosis; vaccine; therapeutic; transgenic; knockout; atherosclerosis; ischaemia; resection; reperfusion injury; sepsis; haematological disease; leukaemia; blood clotting; thrombosis; cancer; tumour; metastasis; inflammatory disease; rhinitis; gastrointestinal disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; respiratory disease; asthma; COPD; chronic obstructive pulmonary disease; respiratory distress syndrome; pulmonary fibrosis; immune disorder; autoimmune disease; rheumatoid arthritis; transplant rejection; allergy; liver disease; cirrhosis; endocrine disease; diabetes; bone disease; osteoporosis; neurological disease; stroke; multiple sclerosis; spinal cord injury; burn; wound healing; infection; cell-cell adhesion; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 373..503 /note= "AD55 adhesion molecule region"

XX Region 376 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 380, 440 and 469"

XX Region 378 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 380, 440 and 469. Also represents a metal ion ligand along with residues 380 and 469"

XX Region 380 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

XX Region 440 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

XX Region 440 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

XX Region 440 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

XX Region 440 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

XX Region 440 /note= "Forms the metal ion-dependent adhesion site (MIDS) with residues 376, 378, 440 and 469. Also represents a metal ion ligand along with residues 378 and 469"

/note= "Forms the metal ion-dependent adhesion site (MIDAS) with residues 376, 378, 380 and 440. Also represents a metal ion ligand along with residues 378 and 380"

WO200262845-A2.

15-AUG-2002.

11-JAN-2002, 2002WO-GB000107.

11-JAN-2001; 2001GB-00000750.

(INPH-) INPHARMATICA LTD.

Gutteridge A, Pagan RJ, Phelps CB;

WPI; 2002-636584/68.

N-PSDB; ABS52589.

New polypeptides comprising adhesion molecules (NCBI Genebank AAC74854.1, AAC76768.1 and P10155), useful for treating, preventing or diagnosing inflammation (e.g. rhinitis), cancers or neurological diseases (e.g. stroke).

Claim 1; Fig 23; 125pp; English.

The invention discloses human adhesion molecule polypeptides (designated AD5a), AD5b and AD5c which have the NCBI Genebank accession numbers, AAC74854.1, AAC76768.1 and P10155, respectively.

Adhesion molecules are involved in a wide range of biological processes from embryogenesis to apoptosis. They are essential to the structural integrity and homeostatic functioning of most tissues and, therefore, defects can play a role in many disease processes. Alteration of their activity is a means to alter the disease phenotype. The polynucleotides and polypeptides can be used to identify ligands that bind specifically to, and which preferably inhibit, the adhesion molecule activity, to identify compounds that either increase or decrease the level of expression or activity, for diagnosing a disease in a patient, in a pharmaceutical composition, as a vaccine, for monitoring the therapeutic treatment of disease in a patient, for creating transgenic or knockout animals, expressing higher, lower or absent levels of the AD5 polypeptide and for screening a compound effective for treating a disease. The AD5 polypeptides, nucleic acids, vectors, ligands, compounds or pharmaceutical compositions, are useful for treating or diagnosing diseases including atherosclerosis, ischaemia, restenosis, reperfusion injury, sepsis, haematological diseases (e.g. leukaemia), blood clotting disorders (e.g. thrombosis), cancer (e.g. lung, prostate, breast, colorectal or brain tumours), metastasis, inflammatory diseases (e.g. rhinitis), gastrointestinal diseases (e.g. inflammatory bowel disease, ulcerative colitis or Crohn's disease), respiratory diseases (e.g. asthma, chronic obstructive pulmonary disease (COPD), respiratory distress syndrome or pulmonary fibrosis), immune disorders (e.g. autoimmune diseases, rheumatoid arthritis, transplant rejection or allergy), liver diseases (e.g. cirrhosis), endocrine diseases (e.g. diabetes), bone diseases (e.g. osteoporosis), neurological diseases (e.g. stroke or multiple sclerosis), spinal cord injury, burns and wound healing or infections (e.g. bacterial infections, particularly Escherichia coli infection). The AD5 polypeptide is particularly useful as an adhesion molecule or for effecting cell-cell adhesion. The protein sequence presented is the human adhesion molecule, termed P10155 (Ro60 or AD55)

Sequence 538 AA;

Query Match 100.0%; Score 2787; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 4,2e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEEVSNQNPINERKQIANSOGYVQVTDNRRLRFLCFSGSGGTYYIKKQGLIENNA 60

1 MEEVSNQNPINERKQIANSOGYVQVTDNRRLRFLCFSGSGGTYYIKKQGLIENNA 60

61 LIRLIEDGRGCEVIOEIKSFQSGRTTKQEPMLFALICSGQSDISTKQAAFKAVSEVCR 120

61 LIRLIEDGRGCEVIOEIKSFQSGRTTKQEPMLFALICSGQSDISTKQAAFKAVSEVCR 120

121 IPTHLFFTIQPKDKLKSMMCGWGRALRAIDWYNEKGMALALAVTKYKQNGSHK 180

121 IPTHLFFTIQPKDKLKSMMCGWGRALRAIDWYNEKGMALALAVTKYKQNGSHK 180

181 DLRLSHLKRSSRGIAIVTKYITKGWKEVHELKXKALSVETBKLLKYLEAVEYKRTKD 240

181 DLRLSHLKRSSRGIAIVTKYITKGWKEVHELKXKALSVETBKLLKYLEAVEYKRTKD 240

241 ELEVIHLIEHRILVREHLITNHLKSKEWKALLQEMPLTALRLNGHOTANSVLEPNSG 300

241 ELEVIHLIEHRILVREHLITNHLKSKEWKALLQEMPLTALRLNGHOTANSVLEPNSG 300

301 VSLVCEKLCNEKLLKARIRHPHILLALETYKTGHGRGLKRRPDEILKALDAARYKT 360

301 VSLVCEKLCNEKLLKARIRHPHILLALETYKTGHGRGLKRRPDEILKALDAARYKT 360

361 FKTYEPTGRKFFLAVDVASMNORVIGSILNASTVAAACGVVTRTKDSYVAFSPDMV 420

361 FKTYEPTGRKFFLAVDVASMNORVIGSILNASTVAAACGVVTRTKDSYVAFSPDMV 420

421 PCPVTIDMTLQOVLNAMSQIPAGTDCSLPMIWAQKNTPADVEIVFTDNETFAGVHPA 480

421 PCPVTIDMTLQOVLNAMSQIPAGTDCSLPMIWAQKNTPADVEIVFTDNETFAGVHPA 480

481 IALREYRKRDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDTGALDIVIRNFTLDM 538

481 IALREYRKRDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDTGALDIVIRNFTLDM 538

RESULT 2

ADR99190 standard; protein; 538 AA.

ADR99190;

02-DEC-2004 (first entry)

Sjogren syndrome antigen A2, SSA2.

Cytostratic; breast cancer; cancer; human; Sjogren syndrome antigen A2;

ribonucleoprotein autoantigen SS-A/Ro; SSA2.

Homo sapiens.

WO2004078035-A2.

16-SEP-2004.

27-FEB-2004; 2004WO-US007268.

28-FEB-2003; 2003US-0450655P.

(FARB) BAYER PHARM CORP.

Evelleigh D, Bigwood D;

WPI; 2004-653556/63.

N-PSDB; ADR99063.

Diagnosing breast cancer comprises comparing the level of expression of genes or gene products in a first biological sample taken from a patient with that in a normal patient sample.

Claim 3; SEQ ID NO 196; 53pp; English.

The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference

in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating breast cancer; and an array for distinguishing between normal and disease tissues comprising two or more probes corresponding to genes selected from ADR98995-ADR99248. In M1 and M2 the genes are selected from ADR98995-ADR99248 and the gene products are polypeptides selected from ADR99121-ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for treating breast cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WFO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 538 AA;

Query Match 100.0%; Score 2787; DB 8; Length 538;

Best Local Similarity 100.0%; Pred. No. 4.2e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEEVNQOPLNEKQIANSQDGYVQVDMNRLHFLCGSGGCTYYIKEQKLGLENAA 60
DB 1 MEEVNQOPLNEKQIANSQDGYVQVDMNRLHFLCGSGGCTYYIKEQKLGLENAA 60
QY 61 LIRLEDGRCGEVIOEIKSFSGEGRTTQOEPMFLALATCSQSDISTKQAKRAVSEVR 120
DB 61 LIRLEDGRCGEVIOEIKSFSGEGRTTQOEPMFLALATCSQSDISTKQAKRAVSEVR 120
QY 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 180
QY 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 180
QY 181 DILRLSHLKPSSBGLAIVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
DB 181 DILRLSHLKPSSBGLAIVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
QY 241 ELEVIHLIEHRLVREHLLTNHLKSKREVKKALLOEMLTALLRNIGKMTANSVLEGENSB 300
DB 241 ELEVIHLIEHRLVREHLLTNHLKSKREVKKALLOEMLTALLRNIGKMTANSVLEGENSB 300
QY 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYTKGHGRLGKLKWRPDEBILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYTKGHGRLGKLKWRPDEBILKALDAAFYKT 360
QY 361 FKTVEPTGKRFLLADVVSASMNQVRVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
DB 361 FKTVEPTGKRFLLADVVSASMNQVRVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
QY 421 PCPVTTDMTLQOVLAMNSQIPAGGTCSLPMTAOCNTTPADVPYFTDNEPAGGVHRA 480
DB 421 PCPVTTDMTLQOVLAMNSQIPAGGTCSLPMTAOCNTTPADVPYFTDNEPAGGVHRA 480
QY 481 IALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGKLDMGCFDTGALDVYRNFTLDMI 538
DB 481 IALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGKLDMGCFDTGALDVYRNFTLDMI 538

```

RESULT 3

AAB46827

ID AAB46827 standard; protein; 552 AA.

AC AAB46827;

XX 26-APR-2001 (first entry)

DE Human antigen SSA60 M4-C6 protein.

XX Antigen; human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;

KW lupus erythematosus; Sjogren's syndrome A.

XX Homo sapiens.
 OS DB19931380-A1.
 XX 11-JAN-2001.
 XX 07-JUL-1999; 99DE-01031380.
 XX 07-JUL-1999; 99DE-01031380.
 XX (HOF) HOFMANN LA ROCHE & CO AG F.
 PI Burchardt J, Haase M, Lehmann H;
 DR WPI, 2001-148274/16.
 XX Recombinant production of ribonucleoprotein, useful for diagnosis of
 PT autoimmune disease, by expressing, in prokaryotes, sequences encoding
 PT both RNA and protein components.

Example 1; Page 13-15; 36pp; German.

This invention describes a novel method for the recombinant production of ribonucleoprotein (I) which comprises producing a prokaryotic host cell that contains at least one DNA (II) encoding an RNA component of (I) and at least one DNA (III) encoding a protein component of (I), expressing both DNAs and then recovering (I). The invention also describes (1) CC nucleic acid constructs containing (II) and (III); (2) recombinant CC prokaryotic cell containing (II) and (III); (3) (I) produced by the new method; and (4) SSA60 protein, designated M56, having a 553 amino acid (aa) sequence, given in the specification, optionally in association with RNA. (I) are used for diagnosis/prognosis of autoimmune diseases, by CC especially systemic lupus erythematosus or Sjogren's syndrome A, by CC complex formation with (I)-specific antibodies. (I) are produced simply, CC inexpensively and on a large scale, in a functional immunologically CC active form that provides a reliable diagnostic test. Complete (I) are CC more selective and sensitive than the protein component used alone, CC whether recombinant or isolated from bovine spleen

Sequence 552 AA;

Query Match 100.0%; Score 2787; DB 4; Length 552;

Best Local Similarity 100.0%; Pred. No. 4.4e-244;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEEVNQOPLNEKQIANSQDGYVQVDMNRLHFLCGSGGCTYYIKEQKLGLENAA 60
DB 13 MEEVNQOPLNEKQIANSQDGYVQVDMNRLHFLCGSGGCTYYIKEQKLGLENAA 72
QY 61 LIRLEDGRCGEVIOEIKSFSGEGRTTQOEPMFLALATCSQSDISTKQAKRAVSEVR 120
DB 73 LIRLEDGRCGEVIOEIKSFSGEGRTTQOEPMFLALATCSQSDISTKQAKRAVSEVR 132
QY 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 180
DB 121 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 192
QY 133 IPTHFTFIOFKKDLKESMKCGMGRALAKAIADWNEKGNALALAVTKYKORNGMSHK 192
DB 181 DILRLSHLKPSSBGLAIVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 240
QY 193 DILRLSHLKPSSBGLAIVTKYITTKGKEVHELYKEKALSVETEKILKYLEAVEKVKRTD 252
QY 241 ELEVIHLIEHRLVREHLLTNHLKSKREVKKALLOEMLTALLRNIGKMTANSVLEGENSB 300
DB 253 ELEVIHLIEHRLVREHLLTNHLKSKREVKKALLOEMLTALLRNIGKMTANSVLEGENSB 312
QY 301 VSLVCEKLCNEKLLKKARLHPHILLALFTYTKGHGRLGKLKWRPDEBILKALDAAFYKT 360
DB 313 VSLVCEKLCNEKLLKKARLHPHILLALFTYTKGHGRLGKLKWRPDEBILKALDAAFYKT 372
QY 361 FKTVEPTGKRFLLADVVSASMNQVRVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 420
DB 373 FKTVEPTGKRFLLADVVSASMNQVRVLSILNASTVAAMCMVVTREKDSYVVAFSDEVY 432

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QY 421 PCPTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAQKNTTPADVIFIVFTDNETFAGVHAPAI 480
 DB 433 PCPTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAQKNTTPADVIFIVFTDNETFAGVHAPAI 492
 QY 481 IALREYRKMDIPAKLIYCGWTSNGFTIADPDDRGMLDMCGFDGTGALDVIRNFTLDMI 538
 DB 493 IALREYRKMDIPAKLIYCGWTSNGFTIADPDDRGMLDMCGFDGTGALDVIRNFTLDMI 550

RESULT 4
 AAB46829 ID AAB46829 standard; protein; 553 AA.
 AC AAB46829;
 DT 26-APR-2001 (first entry)
 DE Human antigen construct pEQ30-HY3-SSA60W56 #4 protein.
 KM Antigen; human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;
 KM lupus erythematosus; Sjorgen's syndrome A.
 OS Homo sapiens.
 PN DE19931380-A1.
 PD 11-JAN-2001.
 PE 07-JUL-1999; 99DE-01031380.
 PF 07-JUL-1999; 99DE-01031380.
 PR 07-JUL-1999; 99DE-01031380.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Burkhardt J, Haas M, Lehmann H;
 DR WPI; 2001-148274/16.
 DR N-PSDB; AAF26157.

Recombinant production of ribonucleoprotein, useful for diagnosis of autoimmune disease, by expressing, in prokaryotes, sequences encoding both RNA and protein components.

Example 1; Page 22-24; 36pp; German.

This invention describes a novel method for the recombinant production of ribonucleoprotein (I) which comprises producing a prokaryotic host cell that contains at least one DNA (II) encoding an RNA component of (I) and at least one DNA (III) encoding a protein component of (I), expressing both DNAs and then recovering (I). The invention also describes (1) nucleic acid constructs containing (II) and (III); (2) recombinant prokaryotic cell containing (II) and (III); (3) (I) produced by the new method; and (4) SSA60 protein, designated M56, having a 553 amino acid sequence, given in the specification, optionally in association with RNA. (I) are used for diagnosis/prognosis of autoimmune diseases, especially systemic lupus erythematosus or Sjorgen's syndrome A, by complex formation with (I)-specific antibodies. (I) are produced simply, inexpensively and on a large scale, in a functional immunologically active form that provides a reliable diagnostic test. Complete (I) are more selective and sensitive than the protein component used alone, whether recombinant or isolated from bovine spleen

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 1,3e-243;
 Matches 537; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EESVNOQOPLNEKQIANSQDGYVQVTDNMLRFLFCGSGGTYIYKEQKLGLENABAL 61
 DB 17 EESVNOQOPLNEKQIANSQDGYVQVTDNMLRFLFCGSGGTYIYKEQKLGLENABAL 76

QY 62 IRLIEDRGCEVIOEIKSFQEGRTTKQEBMFLPALAICSCCSDISTKQAFKAVSEVCRI 121
 DB 77 IRLIEDRGCEVIOEIKSFQEGRTTKQEBMFLPALAICSCCSDISTKQAFKAVSEVCRI 136
 QY 122 PTHLFTFIQPKKOLKESMKCGMGRALRKALADWYNEKGMALALAVTKKQNRGSHKD 181
 DB 137 PTHLFTFIQPKKOLKESMKCGMGRALRKALADWYNEKGMALALAVTKKQNRGSHKD 196
 QY 182 LRLSHLKPSSEGLAVYTKITKGWKEVHELYEKLVSFTEKLLKYLAVKVKRTKDE 241
 DB 197 LRLSHLKPSSEGLAVYTKITKGWKEVHELYEKLVSFTEKLLKYLAVKVKRTKDE 256
 QY 242 LEVYHLIEBRLVREHLLTNHLKSKEVWKALQEMPLTALLRNIGKXTANSVLEPGNSEV 301
 DB 257 LEVYHLIEBRLVREHLLTNHLKSKEVWKALQEMPLTALLRNIGKXTANSVLEPGNSEV 316
 QY 302 SLVCEKLCNEKLLKQARIRHFFHLLALEYTKTGHGRLKRPDEEILLQALDAAPFKTF 361
 DB 317 SLVCEKLCNEKLLKQARIRHFFHLLALEYTKTGHGRLKRPDEEILLQALDAAPFKTF 376
 QY 362 KTVBPTGKRFLAVDVSASNNORVLGSLINASTVAAAMCVVTRTEKDSYVAFPSDEMVP 421
 DB 377 KTVBPTGKRFLAVDVSASNNORVLGSLINASTVAAAMCVVTRTEKDSYVAFPSDEMVP 436
 QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAQKNTTPADVIFIVFTDNETFAGVHAPAI 481
 DB 437 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAQKNTTPADVIFIVFTDNETFAGVHAPAI 496
 QY 482 ALREYRKMDIPAKLIYCGWTSNGFTIADPDDRGMLDMCGFDGTGALDVIRNFTLDMI 538
 DB 497 ALREYRKMDIPAKLIYCGWTSNGFTIADPDDRGMLDMCGFDGTGALDVIRNFTLDMI 553

RESULT 5
 AAB46828 ID AAB46828 standard; protein; 553 AA.
 AC AAB46828;
 DT 26-APR-2001 (first entry)
 DE Human antigen SSA60 M56 protein.
 KM Antigen; human; SSA60; ribonucleoprotein; autoimmune disease; diagnosis;
 KM lupus erythematosus; Sjorgen's syndrome A.
 OS Homo sapiens.
 PN DE19931380-A1.
 PD 11-JAN-2001.
 PE 07-JUL-1999; 99DE-01031380.
 PF 07-JUL-1999; 99DE-01031380.
 PR 07-JUL-1999; 99DE-01031380.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Burkhardt J, Haas M, Lehmann H;
 DR WPI; 2001-148274/16.

Recombinant production of ribonucleoprotein, useful for diagnosis of autoimmune disease, by expressing, in prokaryotes, sequences encoding both RNA and protein components.

Claim 15; Page 15-18; 36pp; German.

This invention describes a novel method for the recombinant production of ribonucleoprotein (I) which comprises producing a prokaryotic host cell that contains at least one DNA (II) encoding an RNA component of (I) and at least one DNA (III) encoding a protein component of (I), expressing both DNAs and then recovering (I). The invention also describes (1)

CC nucleic acid constructs containing (II) and (III); (2) recombinant
 CC prokaryotic cell containing (II) and (III); (3) (1) produced by the new
 CC method; and (4) SSA60 protein, designated M56, having a 553 amino acid
 CC (aa) sequence, given in the specification, optionally in association with
 CC RNA. (I) are used for diagnosis/prognosis of autoimmune diseases,
 CC especially systemic lupus erythematosus or Sjogren's syndrome A, by
 CC complex formation with (I)-specific antibodies; (I) are produced simply,
 CC inexpensively and on a large scale, in a functional (immunologically
 CC active) form that provides a reliable diagnostic test. Complete (I) are
 CC more selective and sensitive than the protein component used alone,
 CC whether recombinant or isolated from bovine spleen

XX Sequence 553 AA;

Query Match 99.8%; Score 2782; DB 4; Length 553;

Best Local Similarity 100.0%; Pred. No. 1.3e-243; Mismatches 0; Indels 0; Gaps 0;

Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EESVNOQPLNEKQIANSQDGYVQVDMRLHPLCGSSGGTYYTQEQGLGENEAL 61
 DB 17 EESVNOQPLNEKQIANSQDGYVQVDMRLHPLCGSSGGTYYTQEQGLGENEAL 76
 QY 62 IRLLEDGCGCEVIOEIKSFSGRGRTTKQBPMLFALAIQSCSDISTKQAFKAVSEVCRI 121
 DB 77 IRLLEDGCGCEVIOEIKSFSGRGRTTKQBPMLFALAIQSCSDISTKQAFKAVSEVCRI 136
 QY 122 PTHLFTFQPKDKLSEKMKCGMGRALAKAIADWTNEKGNALALAVTKYKQRNWSHKD 181
 DB 137 PTHLFTFQPKDKLSEKMKCGMGRALAKAIADWTNEKGNALALAVTKYKQRNWSHKD 196
 QY 182 LLRLSHLKPSSEGLAIVTKYITKGEVHELYKEKALSVETBKILKYIAEVEKVKRTQDE 241
 DB 197 LLRLSHLKPSSEGLAIVTKYITKGEVHELYKEKALSVETBKILKYIAEVEKVKRTQDE 256
 QY 242 LEVHLIEEHLVREHLTLNHLKSEKWKALLOEHLRLLRNLGKMTANSVLEPENSEV 301
 DB 257 LEVHLIEEHLVREHLTLNHLKSEKWKALLOEHLRLLRNLGKMTANSVLEPENSEV 316
 QY 302 SLVGEKLCNEKLLKARIRPHILIALETKYTGHLRGKILKMRPDEILKALDAAFYKTF 361
 DB 317 SLVGEKLCNEKLLKARIRPHILIALETKYTGHLRGKILKMRPDEILKALDAAFYKTF 376
 QY 362 KTVBETGGRFLIADVSAWNOGVIGSTINASTVAAACMVTTRREKSYVAEDEVWP 421
 DB 377 KTVBETGGRFLIADVSAWNOGVIGSTINASTVAAACMVTTRREKSYVAEDEVWP 436
 QY 422 CPVTDMTLQOVLAMSGQIPAGGTCSLPMIWAQKTNTPADVFIPTNNEPAGVHPAI 481
 DB 437 CPVTDMTLQOVLAMSGQIPAGGTCSLPMIWAQKTNTPADVFIPTNNEPAGVHPAI 496
 QY 482 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDNGCFPTGALADVIINFTLMI 538
 DB 497 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDNGCFPTGALADVIINFTLMI 553

RESULT 6
 ADRA1766
 ID ADRA1766 standard; protein; 525 AA.
 AC ADRA1766;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Protein sequence of human SS-A/Ro ribonucleoprotein 60 kD autoantigen.
 XX
 KW Human, autoantigen, SS-A/Ro ribonucleoprotein; SS-A;
 KW notch signalling pathway; autoimmune disorder; bystander effect;
 KW suppressor; DSL domain; EGF domain; Goodpasture's disease;
 KW Wegener's granulomatosis; anaemia; thrombocytopenia; gastritis;
 KW hepatitis; vasculitis; scleroderma; myositis; arthritis;
 KW systemic lupus erythematosus; SLE; Sjogren's syndrome; hepatic fibrosis;
 KW liver cirrhosis; thyroiditis; dermatitis; placental dysfunction;
 KW eclampsia; inflammatory related gynaecological disease;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington disease; encephalitis; psychiatric disorder; Down's syndrome;
 KW stroke; exogenous; bystander antigen; multiple sclerosis;
 KW delta serrate leg; inflammatory bowel disease; notch receptor.

OS Homo sapiens.

XX WO2004064863-A1.

XX 05-AUG-2004.

PF 23-JAN-2004; 2004WO-GB000263.

PR 23-JAN-2003; 2003GB-00001510.

PR 23-JAN-2003; 2003GB-00001512.

PR 23-JAN-2003; 2003GB-00001513.

PR 23-JAN-2003; 2003GB-00001515.

PR 23-JAN-2003; 2003GB-00001518.

PR 23-JAN-2003; 2003GB-00001519.

PR 23-JAN-2003; 2003GB-00001521.

PR 23-JAN-2003; 2003GB-00001522.

PR 23-JAN-2003; 2003GB-00001524.

PR 23-JAN-2003; 2003GB-00001526.

PR 23-JAN-2003; 2003GB-00001527.

PR 23-JAN-2003; 2003GB-00001529.

PR 04-APR-2003; 2003WO-GB001525.

PR 24-MAY-2003; 2003GB-00012062.

PR 01-AUG-2003; 2003WO-GB003285.

PR 03-OCT-2003; 2003GB-00023130.

PR 07-JAN-2004; 2004WO-GB000046.

PA (LORA-) LORANTIS LTD.

PI Champion BR, Ragno S, Young LL;

DR WPI, 2004-562091/54.

PT New product having a modulator of the Notch signaling pathway, useful for
 FT modulating an immune response in autoimmune disorders, such as anemia,
 PT gastritis, hepatitis, scleroderma and myositis.

PS Disclosure; Page 112-113; 244pp; English.

CC The invention relates to the modulation of immune function through a
 CC notch signalling pathway for the prevention of autoimmune diseases. It
 CC has been found that the notch signalling pathway provides a bystander
 CC effect or bystander suppression effect, which can be used in a wide
 CC variety of ways to suppress unwanted immune responses in immune diseases
 CC and disorders. Autoimmune diseases are characterised by immune responses
 CC that are directed against self antigens. T lymphocytes are activated upon
 CC recognition of a self antigen and/or a foreign antigen as a complex with
 CC self major histocompatibility complex (MHC) gene products on the surface
 CC of antigen presenting cells (APC). The invention provides the method of
 CC modulating of an immune response, modulator information and a
 CC pharmaceutical kit for suppression of an immune response. The modulator
 CC of the notch signalling pathway is an agent which activates the notch
 CC receptor or a polynucleotide which codes for such an agent. It comprises
 CC a protein or polypeptide comprising a notch ligand DSL (delta serrate
 CC lag) domain, notch ligand EGF domain, optionally all or part of a notch
 CC ligand N terminal domain, and optionally one or more heterologous amino
 CC acid or a polynucleotide sequences. The modulator can be a fusion protein
 CC comprising a segment of a notch ligand extracellular domain and an
 CC immunoglobulin Fc segment. The disorders include Goodpasture's disease,
 CC Wegener's granulomatosis, autoimmune anaemia, thrombocytopenia,
 CC gastritis, autoimmune hepatitis, inflammatory bowel disease, autoimmune
 CC vasculitis, scleroderma, myositis, autoimmune arthritis, Systemic lupus
 CC erythematosus (SLE) or Sjogren's syndrome, hepatic fibrosis, liver
 CC cirrhosis, thyroiditis, dermatitis, placental dysfunction, eclampsia,
 CC inflammatory related gynaecological diseases, neurodegenerative disorders
 CC (such as Alzheimer's disease, Parkinson's disease, Huntington disease)
 CC encephalitis, psychiatric disorders, Down's syndrome, stroke, multiple
 CC sclerosis, etc. The invention discloses a method for generating immune
 CC suppression at a disease locus by administering an exogenous antigen. It

CC also provides the use of modulator or activator of notch signalling in
 CC simultaneous, separate or sequential combination with a bystander antigen
 CC or antigenic determinant for reducing an immune response to a target
 CC antigen. The presented protein sequence is the human SS-A/Ro
 CC ribonucleoprotein autoantigen (60 kD) which is an example of Sjogren's
 CC syndrome autoantigen and bystander antigen.

XX Sequence 525 AA;

Query Match 95.4%; Score 2659; DB 8; Length 525;

Best Local Similarity 99.4%; Pred. No. 1.8e-232;
 Matches 513; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MESSVNQMOPLANEQIANSQDGYWQVTDMMRLHRLFCPSSEGGTYIKOKJGLENAEA 60
DB 1 MESSVNQMOPLANEQIANSQDGYWQVTDMMRLHRLFCPSSEGGTYIKOKJGLENAEA 60
QY 61 LIRLIEGRGCEVIOEIKSPSOEGRTTKOEPMLPALAICQSCSDISTKQAAFKAVSEVCR 120
DB 61 LIRLIEGRGCEVIOEIKSPSOEGRTTKOEPMLPALAICQSCSDISTKQAAFKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMCGMMGRALRAKADWYNEKGMALALAVTKYKQKNGMSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMCGMMGRALRAKADWYNEKGMALALAVTKYKQKNGMSHK 180
QY 181 DLRLSHLKPSSEGLAVTKYITKGWKEVHLYEKALSVETEKLYLAEVKEVKRTRD 240
DB 181 DLRLSHLKPSSEGLAVTKYITKGWKEVHLYEKALSVETEKLYLAEVKEVKRTRD 240
QY 241 ELEVIYHIEHRVREHLITNHLKSEKWKALQEMPLTALLRNIGMTANSVLEPQNSE 300
DB 241 ELEVIYHIEHRVREHLITNHLKSEKWKALQEMPLTALLRNIGMTANSVLEPQNSE 300
QY 301 VSLVCEKLCNEKLIKARIRHPHILIALEYTKGHGRGKUKMRPDEILKALDAARYKT 360
DB 301 VSLVCEKLCNEKLIKARIRHPHILIALEYTKGHGRGKUKMRPDEILKALDAARYKT 360
QY 361 PKTYEPKGRRLAVDVASANNQVLSIINASTVAAMCMVTRTEKDSVVAFSDENV 420
DB 361 PKTYEPKGRRLAVDVASANNQVLSIINASTVAAMCMVTRTEKDSVVAFSDENV 420
QY 421 PCPYTDMTLOQVLMANSQIPAGGTDGSLPMIMAKTKTPADVIVFTDNETFAGVHPA 480
DB 421 PCPYTDMTLOQVLMANSQIPAGGTDGSLPMIMAKTKTPADVIVFTDNETFAGVHPA 480
QY 481 IALREYRKMDIPAKLIYCGMTSNGFTIADPDDRG 516
DB 481 IALREYRKMDIPAKLIYCGMTSNGFTIADPDDRG 516

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RESULT 7
 ADS14359 ID ADS14359 standard; protein; 525 AA.

XX ADS14359;

DT 16-DEC-2004 (first entry)

DE Human SS-A/Ro ribonucleoprotein autoantigen 60 kD subunit.

XX Cytostatic; Immunosuppressive; Antidiabetic; Neuroprotective;
 KW Antiarthritic; Antirheumatic; Antiallergic; Vaccine; Notch signaling;
 KW Notch; Notch ligand; Delta protein; Serrate protein; Jagged protein;
 KW multiple sclerosis; rheumatoid arthritis; diabetes; allergy;
 KW immune disorder; autoimmune disease; graft rejection; cancer;
 KW organ transplant; human; Sjogren's syndrome; SS-A;
 KW Ro ribonucleoprotein autoantigen 60 kD subunit.

OS Homo sapiens.

PN MO200408372-A2.

XX 30-SEP-2004.

XX 22-MAR-2004; 2004MO-GB001229.
 PF 21-MAR-2003; 2003GB-00005582.
 PR 21-MAR-2003; 2003GB-00005583.
 PR 21-MAR-2003; 2003GB-00005621.
 PR 22-MAR-2003; 2003GB-00006622.
 PR 22-MAR-2003; 2003GB-00006624.
 PR 22-MAR-2003; 2003GB-00006626.
 PR 22-MAR-2003; 2003GB-00006640.
 PR 22-MAR-2003; 2003GB-00006644.
 PR 22-MAR-2003; 2003GB-00006650.
 PR 22-MAR-2003; 2003GB-00006651.
 PR 22-MAR-2003; 2003GB-00006654.
 PA (LORA-) LORANTIS LTD.
 XX
 PI Champion BR, Ragno S;
 XX
 DR WPI; 2004-709927/69.

PT Particle capable of being inserted into or taken up by cell useful for
 PT modulating immune response to antigen in subject, comprises
 PT polynucleotide coding for modulator of Notch signaling, and
 PT polynucleotide coding for antigen.

PS Disclosure; Page 162; 278pp; English.

XX The present invention relates to a particle (I) capable of being inserted
 CC into or taken up by a cell comprising (i) a polynucleotide coding for a
 CC modulator of Notch signaling, and (ii) a polynucleotide coding for an
 CC antigen or antigenic determinant. The first polynucleotide sequence codes
 CC for a Notch ligand such as a Delta or Serrate/Jagged protein or its
 CC fragment, derivative, homologue, analogue or allelic variant, or for a
 CC protein which comprises a Notch ligand DSL domain and at least one Notch
 CC ligand EGF-like domain and optionally a membrane binding or transmembrane
 CC domain. The first and second sequences are operably linked to one or more
 CC promoters or enhancers or polyadenylation sequences. The antigen or
 CC antigenic determinant is an allergen, autoantigen, Major
 CC histocompatibility complex (MHC) (transplant) antigen, pathogen antigen,
 CC tumour antigen or their antigenic determinant. (I) is useful for
 CC modulating an immune response to an antigen in a subject. Pharmaceutical
 CC compositions comprising (I) are useful for treating or preventing
 CC conditions mediated by T cells, such as multiple sclerosis, rheumatoid
 CC arthritis, diabetes, allergy, for treating immune disorders such as
 CC autoimmune diseases of graft rejection such as allograft rejection,
 CC treating cancer and organ transplants. The present sequence is human SS-
 CC A/Ro ribonucleoprotein autoantigen 60 kD subunit which is an autoantigen
 CC involved in Sjogren's syndrome and can be used as an antigen to prepare
 CC the particle of the invention.

XX Sequence 525 AA;

Query Match 95.4%; Score 2659; DB 8; Length 525;

Best Local Similarity 99.4%; Pred. No. 1.8e-232;
 Matches 513; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MESSVNQMOPLANEQIANSQDGYWQVTDMMRLHRLFCPSSEGGTYIKOKJGLENAEA 60
DB 1 MESSVNQMOPLANEQIANSQDGYWQVTDMMRLHRLFCPSSEGGTYIKOKJGLENAEA 60
QY 61 LIRLIEGRGCEVIOEIKSPSOEGRTTKOEPMLPALAICQSCSDISTKQAAFKAVSEVCR 120
DB 61 LIRLIEGRGCEVIOEIKSPSOEGRTTKOEPMLPALAICQSCSDISTKQAAFKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMCGMMGRALRAKADWYNEKGMALALAVTKYKQKNGMSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMCGMMGRALRAKADWYNEKGMALALAVTKYKQKNGMSHK 180
QY 181 DLRLSHLKPSSEGLAVTKYITKGWKEVHLYEKALSVETEKLYLAEVKEVKRTRD 240
DB 181 DLRLSHLKPSSEGLAVTKYITKGWKEVHLYEKALSVETEKLYLAEVKEVKRTRD 240

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QY 241 ELEVTNHLIEEHLVREHLITNNHLSKEVWKALLQEMPTALLRNIGKMTANSVLEBGNSE 300
 DB 241 ELEVTNHLIEEHLVREHLITNNHLSKEVWKALLQEMPTALLRNIGKMTANSVLEBGNSE 300
 QY 301 VSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLRGKLMKRPDEELIKALDAAFYKT 360
 DB 301 VSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLRGKLMKRPDEELIKALDAAFYKT 360
 QY 361 PKTVEPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDENY 420
 DB 361 PKTVEPTGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDENY 420
 QY 421 PCPVTDTMTLQOVLAMMSQIPAGGTDGSLPMIWAQKTNTPADVIFVFTDNETPAGGVH 480
 DB 421 PCPVTDTMTLQOVLAMMSQIPAGGTDGSLPMIWAQKTNTPADVIFVFTDNETPAGGVH 480
 QY 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRG 516
 DB 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRG 516

RESULT 8

AAW03717
 ID AAW03717 standard; protein; 413 AA.

AC AAW03717,
 XX 25-MAR-2003 (revised)
 DT 12-MAR-1997 (first entry)
 DE Human autoantigen Ro(SS-A).
 XX Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 KM systemic lupus erythematosus; diagnosis.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT 1. 413
 FT /label= Ro antigen
 FT /note= "X's in the present sequence indicate amino acid
 FT positions given the designation End in the specification"

XX US5541291-A.
 PN 30-JUL-1996.
 PD 27-MAY-1987; 87US-00054871.
 PF 31-DEC-1984; 84US-00687908.
 PR (UYDU-) UNIV DUKE.

XX Keene JD,
 PI WPI, 1996-362015/36.
 DR Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.
 PS Disclosure; Col 15-16; 21pp; English.

XX The human Ro protein is highly common among autoimmune patients. Ro is
 CC characteristic of patients with Sjogren's syndrome and is likely to be a
 CC major pathogenic factor in the foetal heartblock syndrome. Ro cDNA has
 CC been isolated from a human brain library. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 413 AA,
 SQ

Query Match 63.8%; Score 1778; DB 2; Length 413;
 Best Local Similarity 96.9%; Pred. No. 1.8e-152;

Matches 349; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 183 LRSLHAKSSSE---GLAIYTKYTTTKGKRYHELYKEKALSVEREKLLKYLEAVEKVRT 238
 DB 13 LILPLRLPRGRHLPQTGLAIVTKYITTKGKVEHELYKEKALSVEREKLLKYLEAVEKVRT 72
 QY 239 KOELEVHILIEEHLVREHLITNNHLSKEVWKALLQEMPTALLRNIGKMTANSVLEBGN 298
 DB 73 KOELEVHILIEEHLVREHLITNNHLSKEVWKALLQEMPTALLRNIGKMTANSVLEBGN 132
 QY 299 SEVSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLRGKLMKRPDEELIKALDAAFY 358
 DB 133 SEVSLVCEKLCNEKLLKKARLHPHILIALETYKTGHLRGKLMKRPDEELIKALDAAFY 192
 QY 359 KTFKTVETGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDENY 418
 DB 193 KTFKTVETGKRFLLAVDVASASNNQVLSILNASTVAAACMVVTRTEKOSYVAFSDENY 252
 QY 419 MWPCTVDTMTLQOVLAMMSQIPAGGTDGSLPMIWAQKTNTPADVIFVFTDNETPAGGVH 478
 DB 253 MWPCTVDTMTLQOVLAMMSQIPAGGTDGSLPMIWAQKTNTPADVIFVFTDNETPAGGVH 312
 QY 479 PALALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDNCGPDYALDVIRNFTLDM 538
 DB 313 PALALREYRKMDIPAKLIIVCGMTSNGFTIADPDDRGMLDNCGPDYALDVIRNFTLDM 372

RESULT 9

AAB94864
 ID AAB94864 standard; protein; 557 AA.

AC AAB94864,
 XX 26-JUN-2001 (first entry)
 DT Human protein sequence SEQ ID NO:16064.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.
 XX EP1074617-A2.

XX 07-FEB-2001.
 PD 28-JUL-2000; 2000EP-00116126.
 PF 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI, 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

PS Claim 8; SEQ ID NO 16064; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences, and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 CC
 XX Sequence 557 AA;
 SQ
 Query Match 63.4%; Score 1768; DB 4; Length 557;
 Best Local Similarity 99.4%; Pred. No. 2.3e-151;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 194 GLAIVTKYITKGWKEVHELVEKALSVETBEKLLKYLEAVEKVKSKDLEVIHLIEEHL 253
 DB 213 GLAIVTKYITKGWKEVHELVEKALSVETBEKLLKYLEAVEKVKSKDLEVIHLIEEHL 272
 QY 254 VREHLTNHLKSKVWKALLQEMPLTALRNLAGMTANSVLEPNSVSLVCEKLCNEKL 313
 DB 273 VREHLTNHLKSKVWKALLQEMPLTALRNLAGMTANSVLEPNSVSLVCEKLCNEKL 332
 QY 314 LKRAIRHPHLLALEYKKGHGRLKMRPDEBELLKALDAFYKPKVTEPTGKRFLL 373
 DB 333 LKRAIRHPHLLALEYKKGHGRLKMRPDEBELLKALDAFYKPKVTEPTGKRFLL 392
 QY 374 AVDVASAMNORVLSIINASTVAAACMVVTRTEKDSVVAFSDEMPVCPVTTDMTLQOV 433
 DB 393 AVDVASAMNORVLSIINASTVAAACMVVTRTEKDSVVAFSDEMPVCPVTTDMTLQOV 452
 QY 434 LMAWSQIPAGTGDCSLPMWAQKNTNPADVFIVFTDNETFAGVHPAIALREYKKMDIP 493
 DB 453 LMAWSQIPAGTGDCSLPMWAQKNTNPADVFIVFTDNETFAGVHPAIALREYKKMDIP 512
 QY 494 AKLIVCGMTSNGFTIADPDDRGMLDMGSPDNGALDIVIRNFTLDMT 538
 DB 513 AKLIVCGMTSNGFTIADPDDRGMLDMGSPDNGALDIVIRNFTLDMT 557
 RESULT 10
 AAAY22511
 ID AAAY22511 standard; protein; 70 AA.
 XX
 AC AAAY22511;
 XX
 DT 19-OCT-1999 (first entry)
 DE Human RORNP-60K protein.
 XX
 XX Cognate RNA; gene expression regulator; RNA-protein interaction; UI RNA;
 KM autoimmune disease; neoplastic disease; developmental biology;
 KM RNA-associated protein.
 XX
 OS Homo sapiens.
 XX
 PN US5866680-A.
 PN
 PD 02-FEB-1999.
 PD
 PF 07-JUN-1995; 95US-00474753.
 PF
 PR 15-NOV-1989; 89US-00436779.
 PR 12-JUN-1990; 90US-00536943.
 PR 27-DEC-1993; 93US-00173941.

XX (KEEN/) KEENE J D.
 PA (OUER/) QUERY C C.
 PA (BENT/) BENTLEY R.
 PI Bentley RO, Keene JD, Query CC;
 DR WPI; 1999-142012/12.
 XX
 PT Conjugates of UI ribonucleoprotein RNA - with nucleic acid probes,
 PT antigens and antibodies.
 XX
 PS Claim 6; Fig 6; 53pp; English.
 XX
 CC This sequence represents an RNA-associated protein. The invention relates
 CC to a compound of formula (IX): (component Y)-(cognate RNA) where:
 CC component Y is covalently bound to the cognate RNA and is selected from
 CC DNA probes, RNA probes, antigens and antibodies; and the cognate RNA is a
 CC polynucleotide comprising at least the sequence shown in AAX84881 and up
 CC to the sequence of UI RNA. The compounds may have a useful application in
 CC numerous fields, including: regulation of gene expression, RNA-protein
 CC interactions, autoimmune and neoplastic diseases, and developmental
 CC biology
 CC
 XX Sequence 70 AA;
 SQ
 Query Match 13.2%; Score 367; DB 2; Length 70;
 Best Local Similarity 98.6%; Pred. No. 2.7e-25;
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 92 MLFALAIQSCSDISTKQAFKAVSEVCRIPTHLPFEIQPKDLKESMKCGMGRALRKA 151
 DB 1 MLFKAIAICSCSDISTKQAFKAVSEVCRIPTHLPFEIQPKDLKESMKCGMGRALRKA 60
 QY 152 IADWNEKGG 161
 DB 61 IADWNEKGG 70
 RESULT 11
 ABB59719
 ID ABB59719 standard; protein; 641 AA.
 XX
 AC ABB59719;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 5949.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PN
 PD 27-SEP-2001.
 PD
 PF 23-MAR-2001; 2001WO-US009231.
 PF
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (BEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL03822.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 5949; 21bp + Sequence Listing; English.
 PS
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB057737-
 CC AB072072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published_pcc_sequences

XX
 XX
 SQ Sequence 641 AA;

Query Match 6.7%; Score 185.5; DB 4; Length 641;
 Best Local Similarity 19.5%; Pred. No. 2.8e-07;
 Matches 123; Conservative 108; Mismatches 242; Indels 159; Gaps 28;

QY 1 MEESVNMQOPLNE---KOIANSQDG-YWQVTDNRHLHFLCFGS-EGGTYYIKEQKGL 55
 DB 64 MEKEAISNQPLKDEBSKQEPNSEGTAISTPAIDKLRKFCSTGTDDEVYTPALDLV 123
 QY 56 EN-----AEALIRLIJEDGRCGVIOBKSF-----SQEGRTTKQBPMLFALICSCSDI 105
 DB 124 ENNPASLKELCQVSED-----ELVECLISVLGSEPNREQPPRPDPFLILAVFTTCBE 179
 QY 106 SRKQAAFAVAVSVCIPTHLFTPIQKDKESM-KCGMGALKALADVNEKGML 164
 DB 180 KKRNVVRNRFTLTISESDLLFVQLVKKVQQLERKTPENFVRQAVLNMGTIK-SLDR 238
 QY 165 ALAVTKYKORNGM-SHKDLLRLSHLKPS8--EGLAVTKYITKGKVEH-----L 212
 DB 229 LIHPSISIGGNWPMARDLVRLHRYNANFLPEIIAALRLSSPRELSQWDFLPLT 298
 QY 213 YKEKALSVETEKLLKYLE-AVERKVKTKQDELEVI-HLIEHRLVREHLLTNHLSKEW 269
 DB 289 PRETIEGVVKRLTDPEDQISIVKKLSLSEWHPFHLLHDPRLA--HFLIPHMS----Y 352
 QY 270 KALLQEMPTALLRNLGKNTANSVLEPNSVSVCEKCNKLLKKARLHPHLLALE 329
 DB 353 EQLLQKMPRLSRL-----NSRVRPAEQLLDKKQLKASNVPRLLLE-- 395
 QY 330 TYKTGHGLRGKLMRPDEILKAL-----DAAFYK-----TFK 362
 DB 396 -----DKRLRKPKYVNVOLVLPSSLKKNKTFKPCCATTSFQKASFLHSVEISFG 445
 QY 363 TVEPTGKRPLAVDVASNMQRVLGSLNAS-----TVAAAMCMVTRTEKDSYVAF 415
 DB 446 LKVALGR-----LHITLNLQAVLGYLGSPCRSLKYLDALVALGFGYFRSDRKVTVEFW 501
 QY 416 SD---EMVCPPTTMDTLOQVLMASQIPAGGDCSLPMIMKQNT----- 459
 DB 502 HRSRGLKALPWTNMSVSE-----AKTCCB-----NOKVTFHNSRPVFTIDR 546
 QY 460 -----PAVPIVPTDNETPAGGVHP-----AIALREYRKQMDPAKLIVCGM-- 501
 DB 547 PRLALDMQTFDVLVLP6---AARGNENNSKCLAAALMDKREGRNSNAFTIMVSLAQ 603
 QY 502 TSNQPTIADPDRGMLDMCGFDTGALDVIRNF 533
 DB 604 RQRSMYISSGRNENLLECLSDIGHTPLINAF 635

RESULT 12

AAR96038 standard; protein; 719 AA.

XX AAR96038,

XX 24-FEB-1997 (first entry)

DE 80 kD protein.

XX Tetrahymena; 80 kD protein; 95 kD protein; telomerase; telomeric repeat;
 KW RNA coupled protein; chromosome; telomere repeat synthesis; antibody;
 KW immortalised cell; cancer; eukaryotic microbe; inhibitor; gene therapy;
 KW fungal infection; therapy; diagnosis; protozoan infection; somatic cell;
 KW p80; p95.

XX Tetrahymena thermophila.

XX MO9619580-A2.

XX 27-JUN-1996.

XX 18-DEC-1995; 95WO-US016531.

XX 19-DEC-1994; 94US-00359125.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Greider C, Collins K, Kobayashi R, Yang XH, Hemish JM,
 PI Autexier C;

XX WPI; 1996-309594/31.

XX N-PSDB; AAT30867.

XX Telomerase protein and related DNA, antibodies, transgenic cells, etc. -
 PT for diagnosis and treatment of cancer and infection by eukaryotic
 PT microbes, also new telomerase inhibitors.

XX Claim 10; Fig 2; 56pp; English.

XX AAR96038 and AAR96039 represent Tetrahymena 80 kD and 95 kD proteins (p80
 CC and p95), respectively. These proteins are components of telomerase. The
 CC proteins act, when coupled to RNA, to add telomeric repeats (of the
 CC sequence TTGGGG) to stabilise chromosomes. The RNA component provides the
 CC template for the telomere repeat synthesis. Antibodies against these
 CC sequences, can be used as immunoassay reagents for the detection of the
 CC proteins. The antibodies can also be used to identify immortalised cells,
 CC or predispotion to immortalisation, particularly cancer, or to diagnose
 CC a disease caused by a eukaryotic microbe. Inhibitors of these proteins
 CC (and these proteins themselves) can be used for therapy or diagnosis. The
 CC inhibitors can be used to treat infection by fungi and protozoa. As
 CC somatic cells do not generally require telomerase, these inhibitors
 CC should have little or no toxicity to the host. The DNA encoding these
 CC sequences are used to produce the recombinant protein, or to isolate
 CC similar genes from other organisms, while transformed cells can be used
 CC in gene therapy

XX Sequence 719 AA;

Query Match 6.5%; Score 180.5; DB 2; Length 719;
 Best Local Similarity 20.7%; Pred. No. 9.5e-07;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTKQAFVAVSEVCIPTHLFTPIQKDKESMCGMGALKALADVNEKGK 161
 DB 193 CTESQRKKTMYFLS-----VTNKKQMDQTKKKRKENLITKL--QAIKSEDSKRETTD 245
 QY 162 M-----ALALATK--YKORNGMSHNDLLRLSHLK-PSEGLAVTKYITKGKVEH 210
 DB 246 INNVEDAIKALPRAWKTIARQNMK-----KMKAPKIPNSTLSKYL-----FK 293
 QY 211 ELYEKALSVETEKLLKYLEAVEKYRTKQDELEVIH-----LIEHRLVREHLLT 260
 DB 294 DLKCHISEPKERYKILG--KKYKTEBEYKAAFQGSASAPFNPBLAGKMKIEISKT 351
 QY 261 --NHLKSK---EYKALI--QEMPTALLRNLGKNTANSVLEPNSV--SLYCKKCN 310
 DB 352 WENELSAKNTAEVVDNLISNQLPYMMLRNI-----SNILKAGVSDTHSIVINKICE 406
 QY 311 EKLKKARIRHPHLLALETY-----KTGHGLRGK-----KWRPDE 347

XX Claim 20; SEQ ID NO 1046; 1185bp; English.

XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC coding sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33941). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPD at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1094 AA;

Query Match 5.1%; Score 143.5; DB 7; Length 1094;
Best Local Similarity 23.7%; Pred. No. 0.0043;
Matches 82; Conservative 52; Mismatches 115; Indels 97; Gaps 15;

QY 46 YVKEKQKLENAEALIRLEIDGRGCEVIOEIKSFQSGERTTKQEBMFLPALMICSCSDI 105
DB 20 YVKEQRLALA-IDEVYRL-NDAYKKESSSHSTSLFSGSSSTKYDPDIK-----AEI 70
QY 106 STKOAFKAVS-EVCRIPTHL-----FTPIQKDKLKSMMKGMWG----- 145
DB 71 STTRRLRVKGLKRELQSMQKELLYKEGCFETIQ---QIDKMSGGSGSYELSEKALITEL 127
QY 146 RALRKAIADWYNEKGMALALAVTKYK---QNGNSHDL----- 182
DB 128 KSIKRAISSGEKQKQMLQSLAQERPHLDQNGISEPDLRCSPVNSHLCLSRQTLDA 187
QY 183 -----LRLSHKPSSEGLAI-VTKYITTKMKVEHYLYEKA 217
DB 189 SQTSTISGDIQVRSNIAEKVRLSLQYBAKRSMAWIKELSLQDSEAPGALDIKEKA 247
QY 218 LSV-ETREKLLKYEAVERKTKQDELEVIHLIEHRLVREHL-----LTNHLKSKE 267
DB 248 MLINKESELKELIQFTYPPQKTKQDELEERLE-AERQRLBELLSVKGTPSALAERLER 306
QY 268 VWEKALQEMPLETALL-----RNIGKRYTANSV-LEPGNSEVSLCEK 307
DB 307 RRRELLQKLEETTKLITVYLSQLKSLASASTLSMSSGSLASASR 352

RESULT 15

ADQ17289 ID ADQ17289 standard; protein; 1937 AA.

XX AC ADQ17289;

XX DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 106.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX MO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Gineburg WM, Zlotnick A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.

XX Example 2; SEQ ID NO 106; 210bp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 1937 AA;

Query Match 4.7%; Score 130.5; DB 8; Length 1937;
Best Local Similarity 20.0%; Pred. No. 0.16;
Matches 101; Conservative 72; Mismatches 168; Indels 165; Gaps 18;

QY 1 MEESVNOQMPLEKQ-----IANSQDGVVQVTDNRLHRLFCGSEGGTY 47
DB 1255 LEDQVSELTKEEEOQRLINDITQAPARIQTAGVYSQIDKDALVSLSSKQASTQ 1314
QY 48 IKQKQKLENN-----ABALIRLEIDGR-GCEVIOEIKSFQSGERTTKQEBMFLPALMICSC 102
DB 1315 IELHQLEEBERKAKNALALHQSNDHCDLLREQYEEBQEKALQ----- 1361
QY 103 STSTKOAFKAVSEVCRIPTHLFT-PIQPKDKLKE-----SMKCG 142
DB 1362 -----RALSKANSEVAQWRTYETDAILQRTLELEBAKKQLAQRLQEAHEVAVANAKA 1415
QY 143 MNGRALRKAIADWYNEKGMAL-----ALAVTKYKORN-----GWSHK----- 180
DB 1416 -----SLEKTKQRLQNEVEDMLDVERSNACALDKQKQNPDKVASEMKQKYEYQAELE 1471
QY 181 -----DLRLSHL-----KPSSEGLAIVTKYITTKMKVEHYLYK 214
DB 1472 ASQKRSRLSTELFKYKQVYVESLDQLETFLREKNKIQOEISDLPFOIAEGGQIHLEBK 1531
QY 215 EKALSVETEKLLKYEAVERKTKQDELEVIHLIEHRLVREHLTNHLKSKEVWQALLQ 274
DB 1532 IKK-QVEQEK-----EIOALAEAEASLEHEBGKTIKRIQLBELNVKSEVDRKTIAR 1582
QY 275 EMPITLALLANIGQM--TANSVLEPG-----NSEVSLVCEK 307

Db 1583 DEIDQKRNTRVETMSTLDAIRSRNDALRVKKKMGEDLNEMEIQLNHNRLAAS 1642
QY 308 LCN---EKLIKARIRHPHILIALETYKTGHGKIKRPPDEILK---ALDAFYK 359
Db 1643 LRNYRNTOGILKETOLH-----LDDALRGQEDLKEQLAIVERRANLIQAEIEE 1690
QY 360 TPKTVEPTGKRFLAVDVASAMNORV 385
Db 1691 LWATTEOTERSRKIAEQELLDASERV 1716

Search completed: January 13, 2006, 11:09:15
Job time : 82 secs

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OM protein - protein search, using SW model

Run on: January 13, 2006, 11:07:29 ; Search time 26 Seconds
(without alignments)
1710.751 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2784	99.9	542	2	US-09-949-016-10805 Sequence 10805, A
2	180.5	6.5	699	2	US-08-851-843A-52 Sequence 52, App1
3	180.5	6.5	699	2	US-08-974-549A-188 Sequence 188, App1
4	180.5	6.5	699	2	US-08-854-050-52 Sequence 52, App1
5	180.5	6.5	699	2	US-09-430-323-52 Sequence 52, App1
6	180.5	6.5	699	2	US-09-402-181B-188 Sequence 188, App1
7	180.5	6.5	699	2	US-09-721-456-188 Sequence 188, App1
8	180.5	6.5	699	2	US-09-766-253-52 Sequence 52, App1
9	180.5	6.5	699	2	US-10-054-295-52 Sequence 52, App1
10	180.5	6.5	699	2	US-09-438-486A-52 Sequence 52, App1
11	180.5	6.5	719	2	US-08-851-843A-7 Sequence 7, App1
12	180.5	6.5	719	2	US-08-974-549A-219 Sequence 219, App1
13	180.5	6.5	719	2	US-08-854-050-7 Sequence 7, App1
14	180.5	6.5	719	2	US-09-430-323-7 Sequence 7, App1
15	180.5	6.5	719	2	US-09-402-181B-219 Sequence 219, App1
16	180.5	6.5	719	2	US-09-721-456-219 Sequence 219, App1
17	180.5	6.5	719	2	US-09-766-253-7 Sequence 7, App1
18	180.5	6.5	719	2	US-10-054-295-7 Sequence 7, App1
19	180.5	6.5	719	2	US-09-438-486A-7 Sequence 7, App1
20	130.5	4.7	1937	2	US-09-538-092-918 Sequence 918, App1
21	123	4.4	23	2	US-08-475-955-48 Sequence 48, App1
22	123	4.4	23	2	US-07-867-819D-48 Sequence 48, App1
23	118	4.2	713	1	US-08-484-993B-2 Sequence 2, App1
24	118	4.2	713	1	US-08-484-158B-2 Sequence 2, App1
25	118	4.2	713	1	US-08-484-596A-2 Sequence 2, App1
26	118	4.2	713	1	US-08-480-150A-2 Sequence 2, App1
27	118	4.2	713	2	US-08-458-731-2 Sequence 2, App1

28	118	4.2	713	2	US-08-149-223A-2	Sequence 2, App1
29	116	4.2	21	2	US-08-716-249-11	Sequence 11, App1
30	116	4.2	22	2	US-08-475-955-55	Sequence 55, App1
31	116	4.2	22	2	US-07-867-819D-55	Sequence 55, App1
32	115.5	4.1	550	2	US-10-104-047-3495	Sequence 3495, App1
33	113.5	4.1	1802	2	US-09-949-016-11073	Sequence 11073, App1
34	113	4.1	1939	2	US-09-538-092-915	Sequence 915, App1
35	113	4.1	1939	2	US-09-949-016-11104	Sequence 11104, App1
36	110.5	4.0	709	2	US-09-328-352-5172	Sequence 5172, App1
37	110.5	4.0	1979	2	US-09-949-016-5468	Sequence 5468, App1
38	110.5	4.0	2047	2	US-09-949-016-7404	Sequence 7404, App1
39	110.5	4.0	2186	2	US-09-949-016-10828	Sequence 10828, App1
40	110.5	4.0	2349	2	US-09-538-092-914	Sequence 914, App1
41	110	3.9	952	2	US-09-248-796A-20878	Sequence 20878, App1
42	110	3.9	1002	2	US-09-620-405B-475	Sequence 475, App1
43	110	3.9	1002	2	US-09-604-287A-475	Sequence 475, App1
44	110	3.9	1002	2	US-09-834-759-475	Sequence 475, App1
45	110	3.9	1002	2	US-09-590-751A-475	Sequence 475, App1

ALIGNMENTS

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RESULT 1
US-09-949-016-10805
Sequence 10805, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10805
LENGTH: 542
TYPE: PRT
ORGANISM: Human
US-09-949-016-10805
Query Match 99.9%; Score 2784; DB 2; Length 542;
Best Local Similarity 99.8%; Pred. No. 2.3e-258;
Matches 537; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 MEEVNMQPLNEKQIANSQDGYVQVTDNMRHRLFCGSEGGTYIYKQKLGLENAA 60
5 MEEVNMQPLNEKQIANSQDGYVQVTDNMRHRLFCGSEGGTYIYKQKLGLENAA 64
61 LIRLIEDGCGCVIOEIKSFSGEGRTTQOEPMFLALITSCQSDISTKAAKAVSEVR 120
LIRLIEDGCGCVIOEIKSFSGEGRTTQOEPMFLALITSCQSDISTKAAKAVSEVR 124
121 IPTHLPFTFOFKKDKESKCGMGRALRKADADYNEKGMALALAVTKYKORNGMSHK 180
IPTHLPFTFOFKKDKESKCGMGRALRKADADYNEKGMALALAVTKYKORNGMSHK 184
125 IPTHLPFTFOFKKDKESKCGMGRALRKADADYNEKGMALALAVTKYKORNGMSHK 184
IPTHLPFTFOFKKDKESKCGMGRALRKADADYNEKGMALALAVTKYKORNGMSHK 188
181 DLRLSHLRKPSSEGLAVTKYITKGKVEHRLYKFKALSVETKLLKYLAVERKRTYD 240
DLRLSHLRKPSSEGLAVTKYITKGKVEHRLYKFKALSVETKLLKYLAVERKRTYD 244
185 DLRLSHLRKPSSEGLAVTKYITKGKVEHRLYKFKALSVETKLLKYLAVERKRTYD 244
DLRLSHLRKPSSEGLAVTKYITKGKVEHRLYKFKALSVETKLLKYLAVERKRTYD 248
241 ELEVIHLIEHRLVREHLLTNHLKSKVKKALLQEMPTALLRNIGKATANSVLEPGNSE 300
ELEVIHLIEHRLVREHLLTNHLKSKVKKALLQEMPTALLRNIGKATANSVLEPGNSE 304
245 ELEVIHLIEHRLVREHLLTNHLKSKVKKALLQEMPTALLRNIGKATANSVLEPGNSE 304
ELEVIHLIEHRLVREHLLTNHLKSKVKKALLQEMPTALLRNIGKATANSVLEPGNSE 308
301 VSLVCKLCKNEKLIKKARLHPHILLALFTYKTHGRLGKLKWRPDEITLKALDAAFYKT 360
VSLVCKLCKNEKLIKKARLHPHILLALFTYKTHGRLGKLKWRPDEITLKALDAAFYKT 364
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Db      305 VSLVCEGLCHKEKLRKRIHPHILILALETYKTHGRLGRLKMRPDEIILKALDAAYTK 364
Qy      361 FKTYEPFGKPEFLADVVSASHNQRVLGSIINASTVAAAMCVVTRTEKDSYVAFSPDEMY 420
Db      365 FKTYEPFGKPEFLADVVSASHNQRVLGSIINASTVAAAMCVVTRTEKDSYVAFSPDEMY 424
Qy      421 PCPTTMTTLOQVLMASQIPAGGTDGSLPMTMAOKTNPADVIVFTDNETFAGVHPA 480
Db      425 PCPTTMTTLOQVLMASQIPAGGTDGSLPMTMAOKTNPADVIVFTDNETFAGVHPA 484
Qy      481 IALREYRKMDIPAKLIYCGTNSGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 538
Db      485 IALREYRKMDIPAKLIYCGTNSGFTIADPDDRGMLDMCGFDGALDVIRNFTLDMI 542

RESULT 2
; Sequence 52, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; JUS-08-851-843A-52

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Query Match      6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3,6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Qy      102 CSDISTKQAFKAVSEVCRIPTLFTFIQPKDLKESMCKGMGRALKAIDATYNEKG 161
Db      175 CTSSQRKKTFRYLS-----VTNKQKWDQTKKGRKENLTKL--QAIKESDSKRETD 227
Qy      162 M-----ALALAATK--YKQRNGSHKDLKLSHK--PSSEGLAVTKYITGMKEVH 210
Db      228 IMMVEDAIKRLKAVMKKIAKRONAMK-----KMKAKKIPNSTLESKYL-----FK 275
Qy      211 ELVKEKALSVTEKTLKYLEAVEKVKRTKDELEVIH-----LIBHRLVREHLT 260
Db      276 DLTKFCHISEPKERVYKILG--KPYKTEEEYKRAFSDSASAPNPFLAGKMKIEISK 333
Qy      261 --NHLKSK---EYWKAL--QEMPLTALRLNGKMTANSVLBPGNSEV--SLVCEKLCN 310
Db      334 MENELSAKNGTAEVMDLISNQLPYVAMLRNL-----SNILKAGVSDTTHSYVINKICE 388
Qy      311 EKLKARIRHPHILILALETY-----KTGHLGRLK-----KMRPDE 347
Db      389 PKAVENSKMFPLOFFSAIEAVNEAVTKGFYAKGRENNMLKGQIEAVKEVEKTDDEKDM 448
Qy      348 ELKALDAAFYKTEKTEPFGKPEFL-----LAV-----DVSASNNQR 384
Db      449 ELEGTEGEF--VKNEGIGKQYINSIELAIKIAVNKNLDEIKGHRIRISDVSGSMSTS 505
Qy      385 VLGSILNASTVAAAM-----CMVYTRTEKDSYV--AFSPDEMYPCPVTTDM----- 428
Db      506 MSGGAKKYGSVRCLECALVIGLAVKQRCEKSFYRSPSSQCNKCYLEVDLPGDELRLP 565
Qy      429 TLQOVLMASQIPAGGTDGSLPMT--WAOKTNPADVIVFTDNETFAG--GVHP 479
Db      566 SMOGLLOEKGL--GGGDPPEYECIDEWT--KMKTHVDIVILSDMLAEGVSDINVRSSI 623
Qy      480 AIDLREYRKMDIPAKLIYCGTNSG--FTIADP--DDRGLMDMCGFDGAL----- 527
Db      624 VNSIKKTYDEVNRIKIFAVDLBEGYKCLAGDEFNENNTYKIFGMSDILKFTSAQGG 683
Qy      528 ----DVIRNFTLDMI 538
Db      684 ANMVEVINKFALOKI 698

RESULT 3
; Sequence 188, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: NO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-188

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Query Match 6.5%; Score 180.5; DB 2; length 699;
Best Local Similarity 20.7%; Pred. No. 3,6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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102 GSDISTKQAAFAVSEVCHLPTFLPFIQPKDKESMKCGMKGRALRAIDMWNKGG 161
175 CTESQKRTKMTFRLS-----VTNKQKMDTKKKRKNLLTKL--QAIKSEDSKKETED 227
162 M-----ALALATK--YKQNGWSHKDLALSHLK--PSSEGLAIVTKYTKGKEVH 210
228 INNVDAITALKRAVWVKTIKAKQNAK-----KMKAPKIPNSTLSEKYL-----PK 275
211 ELYKEKALSVETEKALKYLEAVEKVRKTQDELEVIH-----LIEBHRLVREHLIT 260
276 DLIKFCHISBPKEKRYVKILG--KKYPTKEBYKAAFGDSASAPFNDELAKKMKIISXT 333
261 --NHLKSK---EVMKALL--QEMPLTALLRNKGKNTANSVLERGSEV--SLVCEKLN 310
334 WENELSAKGNJAEVWNLISNQLPYMAMRLN-----SNILKAGVSDTHSIVINKICB 388
311 EKLKKARLHPHILALETY-----KTGHGLRGKL-----KWRPDE 347
389 PKAVENSKMPPLQPFSAIEAVNAVATKGFPAKKGKEMNTLKGQIEAVKEVVEKTDKKDM 448

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348 EILKALDAAFYKTEPTVETGRFL-----LAV-----DVASAMNQR 384
449 ELEQTEEEEF---VKANEGIKQYINSIELAKIAVNKNLDEIKGHTAIFSDVSGSMST 505
385 VLGSILNASTVLAAM-----QAVTTEKOSIVV--AFSDENVPCEVTTDM----- 428
506 MSGAKKYGVSRTCLCALVGLMWKQRCESKSFYFSSPSCNCKTLEVDLPDELRP 565
429 TLOOVLAAMSQIPAGCTDCLPMI--MAQKNTPADVFIVFTDNETFAG-----GVHP 479
566 SMOKILOEKGLD-GGGTDPPYECIDEWL--KKTHVDNIVILSDMVIAGYSDINVRGSI 623
480 AIALREYKQMDIPAKLIVCGMTSNG--FTIADP--DGRGMLDMCGFDTGAL----- 527
624 VASIKKYDEVNPNIKIYAVDLEGGYKGLNIGDERENNYYIKIGMSDILKFIKAKGG 683
528 ---DVIRNFTLDMI 538
684 ANWVEVIGNFALQKI 698

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RESULT 4
US-08-854-050-52
Sequence 52, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Langner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

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Db 566 SMOCKLOEKGL-GGGTDPYECIDEMT-KNTHVDNIVILSDMMIABGYSDINVRGSSI 623
 Qy 480 AIALREYRKMDIPAKLIYCGWTSNG--FTIADP-DDRGMLDMCGFDYCAL----- 527
 Db 624 VNSIKKYDEVNPNKIRAVDLEGYKCLNLGDEFENNNYIKIFGMSDILKFIKAKG 683
 Qy 528 ----DVIRNFTLDMT 538
 Db 684 ANMVEVINKPFLQKI 698

RESULT 6
 US-09-402-181B-188
 ; Sequence 188, Application US/09402181B
 ; Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181B
 FILING DATE: 29-Sep-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17895
 FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausehus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 188:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 699 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 188:
 US-09-402-181B-188

Query Match 6.5%; Score 180.5; DB 2; Length 699;
 Best Local Similarity 20.7%; Pred. No. 3.6e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Qy 102 CSDISTKQAFKAVSEVCRIPTHLFTPIQFKDLKESKCGMGRALKALADWNEKG 161
 Db 175 CTESQKKTWFRYLS-----VTNKKMDQTKKKRENNLTGL--QAIKESDKSKRRTGD 227
 Qy 162 M-----ALALAVTK--YKORNGSHKDLLRLSHLK-PSEGLAIYTKYTKGMKEVH 210
 Db 228 IANVEDAIKALKPAWKRIARQNNMK-----KMKAPKIPNSTLSKTLT-----FK 275
 Qy 211 ELYKEKALSVETEKLLKYLAWEKVKRTKDELEVH-----LIEHRLVREHLLT 260
 Db 276 DLKCHHSBKERYKYLIG--KKYPTBEYKAFGSASAPFNPBLAGKRMKIEISKI 333
 Qy 261 --NHLKSK---EWKALL--QEMPYLALNNGKMTANSVLEPNSGV--SLVCEKLCN 310
 Db 334 WENELSAKNTAEVWDNLISNQLEPYMAMRLNL-----SNILKAGVSDTHSIVINKICE 388
 Qy 311 EKLKKAIRPHILIALETY-----KTHGLRGTL-----KMRPDE 347
 Db 389 PAVAVNSKQFLOPFSALBAVNEAVTKGFKAKGRNNMLKQIABKVEKTEDEKCDM 448
 Qy 348 BILKALDAFYKTFKVEPTGRFL-----LAV-----DVSASMQR 384
 Db 449 ELEQTEBGEF--VKNVIGIKQYINSIEIAKIAVKNKIDBIKHTAIFSDVSGSMST 505
 Qy 385 VLGSTINASTYAAAN-----CMVVTREKDSYV--AFSDENVPCPYTDM----- 428
 Db 506 MSGAKKCVGVATGECALVIGLAWKORCEKSFYIFSSSQCKCYLEVLDLPGDELRLP 565
 Qy 429 TLQOVLAMSQIPAGTDCSLPMI--VAQKNTTPADVPIVFTDNTDFG-----GVHP 479
 Db 566 SMOCKLOEKGL-GGGTDPYECIDEMT-KNTHVDNIVILSDMMIABGYSDINVRGSSI 623
 Qy 480 AIALREYRKMDIPAKLIYCGWTSNG--FTIADP-DDRGMLDMCGFDYCAL----- 527
 Db 624 VNSIKKYDEVNPNKIRAVDLEGYKCLNLGDEFENNNYIKIFGMSDILKFIKAKG 683
 Qy 528 ----DVIRNFTLDMT 538
 Db 684 ANMVEVINKPFLQKI 698

RESULT 7
 US-09-721-456-188
 ; Sequence 188, Application US/09721456
 ; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0280
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-721-456-188

Query Match          6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAPKAVSEVCRIPTLHPTFQPKDLKESKCGMGRALKAIADYNEKG 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 CTESQARKTMYRYS-----VTNKOQMDQTKKREKENTLTL--QAIKESDKSKRETD 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 162 M-----ALALAVTK--VKORNGMSHKDLRLSLHK-PSEGLAIYTKYITGWEVH 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 IANVEDAIKALKAPAMKIAKRONAMK-----KMKAPKIPNSTLESKLT-----FK 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 211 ELYEKALSVETELKLTLYLAVERKVKRDELEVIH-----LIEEHLVREHLLT 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 DLIFCHISEKKEVYKILG--KKYPTKEEYKAFGDSASAPNPBLAGKRMIEISKT 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 261 --NHLKSK---EYWKAL--QEMPLTLLNNGMTANSLVPGNSEV--SLYCEKLCN 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 334 WENELSAKGNATFAVWDNLISNOLPYMAMLRNL-----SNIKAGVSPYTHSIYINICE 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 311 EKLLAKARIHFIHLIALEY-----KTHGLRGKL-----KMRPDE 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 PKAVENSMPLOPSPSAIEAVNATKGFKAKKRENNMLKGQIEAVKEVEKTDKCKDM 448
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 348 EILKALDAAFKTEVPTGKRFV---LAV-----DVSAMNOR 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 449 ELBQTERGEF---VKVNEGIGQYINSIELAIKIAVNRKNDLKGHTAIFSDVSGSNSTS 505
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 385 VLGSILNASTVAAM-----GVVYTRTEKDSYV--AFSDENVPCTPTDM----- 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 506 MSGAKKYGSGVRCTCEBALVGLMVKORCEKSSFYIFSSSQCNKCYLEVDLPGDELRP 565
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 429 TLQOVLAMASQIPAGGDCSLPMI--WAQRTNPADVFIVFTDNETPAG-----GVHP 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 SMQKTLQEKKL-GGGIDPEYECIDEWT-KNKTHTVDIVILSDMWLAEGYSDINVRGSSI 623
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 480 AIALREYRKMDIPAKLIYCGMTSNG--FTIADP-DRGMLDNCGFPTGL----- 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 624 VNSIKKTKQEVNPRIKTFAVDLBYGKCLNLGDEFNENNYIKLFGMSDSILKFIKSAQGG 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Cy 528 ----DVIRNFTLMI 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 684 ANMEVYIKNPLAKTI 698
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-766-253-52
Sequence 52, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin
            Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-766-253-52

Query Match          6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;

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Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTKQAPFAVSEVCRIPHTLFTFIQPKDKLSEKSCGMRALAKAIADWTNEKG 161
 DB 175 CTESQKRTMRYLS-----VTNKQKMDQTKKREKENTLTCL--QAIKESSEKSKRETFGD 227
 QY 162 M-----ALALAVTK--YKQRNWSHKDLRLSLHK-PSSEGLAIVTKYITKGMKEVH 210
 DB 228 IMNVEDAIKALKPAWKKIARQNMK-----KHMKAIPKIPNSTLSKYLT-----FK 275
 QY 211 ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLVNEHLIT 260
 DB 276 DLIFCHISEPERKYKILG--KKYKTEEBEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 QY 261 --NHLKSK---EYWKALL--QEMPLTALLRLGKMTANSVLEPNSSEV--SLVCEKLCN 310
 DB 334 WENELSAKGNATAEVNDLISNQLPYMLRL-----SNLKAGVSDTTHSIVNKICE 388
 QY 311 EKLKKAIRHPHILALETY-----KTGHGLRGKL-----KWRPDE 347
 DB 389 PKAVENSKPFLOFSAIEAVNEAVTKGPKAKRENMLKQDIEAVKEVEKTEDEKDM 448
 QY 348 EILKALDAFYKTFVETGKRP-----LAV-----DVASAMNOR 384
 DB 449 ELEQTEBEF--VKVNEGIGKQYINSIELAIKIVNKLDEIKGHTAIFSDVSGSMST 505
 QY 385 VLGSILNASTVAAAM-----CMVVTREKDSYVV--AFSDENVPCTVTDM----- 428
 DB 506 MSGGAKKYGVSATCECALVIGLWVKORCEKSSFYIFSPSSQCKCYLEVLPDDELRLP 565
 QY 429 TLQOVLAMMSQIPAGTDCSLPMI--MAOKTTPADVTFVFDNETFAG-----GVHP 479
 DB 566 SMQKLOEKGKX--GGTDFPYECIDEMT--KNTIHDNIVILSDMMIABEYSDINRGSSI 623
 QY 480 AIALREYRKMDIPAKLIVCGWTSNG--FTIADP--DDRGMILMCGPDTGAL----- 527
 DB 624 VNSIKKYDEVVNPNIKIFAVDLEGYKCLNLDDEFENNYIKIFGMSDILKFIKAKOG 683
 QY 528 ----DVIRNFTLDM 538
 DB 684 ANNVEVIRKIFALOKI 698

RESULT 9
 US-10-054-295-52
 Sequence 52, Application US/10054295
 Patent No. 6921664
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Langer, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: No. 6921664el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/054,295
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/854,050
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 699 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 52:
 US-10-054-295-52

Query Match 6.5%; Score 180.5; DB 2; Length 699;
 Best Local Similarity 20.7%; Pred. No. 3.6e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 CSDISTKQAPFAVSEVCRIPHTLFTFIQPKDKLSEKSCGMRALAKAIADWTNEKG 161
 DB 175 CTESQKRTMRYLS-----VTNKQKMDQTKKREKENTLTCL--QAIKESSEKSKRETFGD 227
 QY 162 M-----ALALAVTK--YKQRNWSHKDLRLSLHK-PSSEGLAIVTKYITKGMKEVH 210
 DB 228 IMNVEDAIKALKPAWKKIARQNMK-----KHMKAIPKIPNSTLSKYLT-----FK 275
 QY 211 ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLVNEHLIT 260
 DB 276 DLIFCHISEPERKYKILG--KKYKTEEBEYKAFGDSASAPFNPBLAGKMKIEISKI 333
 QY 261 --NHLKSK---EYWKALL--QEMPLTALLRLGKMTANSVLEPNSSEV--SLVCEKLCN 310
 DB 334 WENELSAKGNATAEVNDLISNQLPYMLRL-----SNLKAGVSDTTHSIVNKICE 388
 QY 311 EKLKKAIRHPHILALETY-----KTGHGLRGKL-----KWRPDE 347
 DB 389 PKAVENSKPFLOFSAIEAVNEAVTKGPKAKRENMLKQDIEAVKEVEKTEDEKDM 448
 QY 348 EILKALDAFYKTFVETGKRP-----LAV-----DVASAMNOR 384
 DB 449 ELEQTEBEF--VKVNEGIGKQYINSIELAIKIVNKLDEIKGHTAIFSDVSGSMST 505
 QY 385 VLGSILNASTVAAAM-----CMVVTREKDSYVV--AFSDENVPCTVTDM----- 428
 DB 506 MSGGAKKYGVSATCECALVIGLWVKORCEKSSFYIFSPSSQCKCYLEVLPDDELRLP 565
 QY 429 TLQOVLAMMSQIPAGTDCSLPMI--MAOKTTPADVTFVFDNETFAG-----GVHP 479
 DB 566 SMQKLOEKGKX--GGTDFPYECIDEMT--KNTIHDNIVILSDMMIABEYSDINRGSSI 623
 QY 480 AIALREYRKMDIPAKLIVCGWTSNG--FTIADP--DDRGMILMCGPDTGAL----- 527
 DB 624 VNSIKKYDEVVNPNIKIFAVDLEGYKCLNLDDEFENNYIKIFGMSDILKFIKAKOG 683
 QY 528 ----DVIRNFTLDM 538
 DB 684 ANNVEVIRKIFALOKI 698

RESULT 10
 US-09-438-486A-52

```

; Sequence 52, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: CECCH, THOMAS R.
; APPLICANT: LINGNER, JOACHIM
; APPLICANT: NAKAMURA, TORU
; APPLICANT: CHAPMAN, KAREN B.
; APPLICANT: MORIN, GREGG B.
; APPLICANT: HARLEY, CALVIN
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 223
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: amino acid sequence
US-09-438-486A-52

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Query Match          6.5%; Score 180.5; DB 2; Length 699;
Best Local Similarity 20.7%; Pred. No. 3.6e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAAKAVSEVCRIPTHLFTPIQPKDKESKCMGMRALRKALADVYNEKG 161
Db 175 CTESQRRKTMFRYLS-----VTNRQKMDQTKRKREKENTLTTL--QAIKESDKSKRRTGD 227
Cy 162 M-----ALALAVTK--YKORNGWSHKDLLRLSHLK-PSEGLAIVTKYITKGWKEVH 210
Db 228 IMNVEDAIKALKAPVAKKIAKQKQNAK-----KHMARPIIMPSTLESKILT-----FK 275
Cy 211 ELYEKALSVETEKLLKYLAEVAKVKTQDELEVTH-----LIEHRRLVREHLLT 260
Db 276 DLIRCHISBPKEERYKILG--KKYPTKEEYKAAFQDSASAPFNPBLAGRMKLEISKI 333
Cy 261 --NHILSK-----EYWKALL--QENPILTLNRLGKMTANSVLEQNGSEV--SLYCEKLCN 310
Db 334 WENELISAQNTAEVWDNLISNOLPYMAMLRNL-----SNLKGAVSDTTHSIYINKICE 388
Cy 311 EKLKKKARIHPHILIALEY-----KTGHGIRGKL-----KMRPDE 347
Db 389 PKAVENSGMFPLOFSAIEAVNEAVTKGFYAKKRNMLKQOIAEVKAVVEKTBDEKQDM 448
Cy 348 EILKALDAAFYKTEKVEPTGRFL-----LAV-----DVSAVMNR 384
Db 449 ELBQTEBEGF---VKVNEGIGQYINSIELAKIADVNNLDEIKGHTAIFDVSGSMSTS 505
Cy 385 VLGSILNASTVAAAM-----CMVVTREKDSYVV--AFSDENVPCVTTDM-----428
Db 506 MSGAKKTKGVSRTCECALVGLMWKORCEKSSFYIFSSPSCQKCYLAEVLDLPGDELAR 565
Cy 429 TLQOVTAMSGDIPAGCTCCLPMI--MAQKNTPADVIVITDNTFAG-----GVHR 479
Db 566 SMQKLLQKQKGL--GGGTDFPYECIDEMT--KXKTHVDNVIILSDMKIAGYSDINVRGSSI 623
Cy 480 AIALREYRKMDIPAKLIVCGTNSG--FTIADP--DGRGMLDMCGFDTGAL-----527
Db 624 VNSIKKYDEVNPNKIKIYAVDLLEGYKGLNLDGENENNYYIKIFGMSDILKFTISAKGG 683

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Cy 528 ----DVIRNFTLDMI 538
Db 684 ANNVEYIKNFALOKI 698

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RESULT 11
US-08-851-843A-7
; Sequence 7, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-851-843A-7

```

```

Query Match          6.5%; Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

Cy 102 CSDISTQAAKAVSEVCRIPTHLFTPIQPKDKESKCMGMRALRKALADVYNEKG 161
Db 193 CTESQRRKTMFRYLS-----VTNRQKMDQTKRKREKENTLTTL--QAIKESDKSKRRTGD 245
Cy 162 M-----ALALAVTK--YKORNGWSHKDLLRLSHLK-PSEGLAIVTKYITKGWKEVH 210

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Db      246  IANVEDAIKALKPAMVKIARQNMK-----KHMAPKIPNSTLESKILT-----FK 293
Qy      211  ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLYREHLIT 260
Db      294  DLIFCHISEPERKENVYKILG--KKYKTEEBEYKAFGDSASAPFNPBLAGRMKIEIKT 351
Qy      261  --NHUKSK-----EYWKALL--QEMPLTALLNLGKMTANSVLEPNSSEV--SLVCEKLCN 310
Db      352  WENELSAAGNTAEVWDNLISSNQLPYMAMLRNL-----SNLIKAGVSDTTHSIVINKICE 406
Qy      311  EKLKKARHPHILIALETY-----KTGHGLRGKL-----KWRPDE 347
Db      407  PRAVENSMPFLQFSPSAIEAVNEAVTKGFKAKGRNNMLKQGLIENVKVEKTEDEKKDM 466
Qy      348  EILKALDAAFYKTFKVEPTGRPL-----LAV-----DVSASMNOR 384
Db      467  ELEQTEEBGEF---VKNVNGIGKQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTS 523
Qy      385  VLGSLINASTVAAMN-----CMVVTREKDSYVV--AFSDENVPCVTTDM----- 428
Db      524  MSGGAKKYGVSRTCECALVIGLWVKORCEKSSFYIFSSPSQCNKCYLEVDLPEDDELRP 583
Qy      429  TLQOVLAMMSQIPAGTDCSLPMI--WAKKNTTPADVPIVFTDNETFAG-----GVHP 479
Db      584  SMOKLQERKGL--GGGTDPPYECIDEMT--KNKTHVDNIVILSDMMIAGYSDINVRGSSI 641
Qy      480  AIALREYKQMDIPNCLIVCGMTSNG--FTIADP--DGRGMLDMCGFDTCAL----- 527
Db      642  VNSIKYKDEVPNPKIFAVDLLEGYKCLNLGDBENNNYIYIFQMSDSILKFTISAKQGG 701
Qy      528  ---DIVRNFITLDMT 538
Db      702  ANMVEVINKPAPLOKI 716

```

RESULT 12
US-08-974-549A-219
Sequence 219, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Czech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-219

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Query Match 6.5%; Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

```

Qy      102  CSDISTQAAFAKVAEVRIPHTLPTFIOFKKDKESKKCGMMGRALKALADATYNEKGG 161
Db      193  CTESQKKTKMFRYLS-----VTNKKQWQTKKGRKENLITKL--QALKESEKSGREYGD 245
Qy      162  M-----ALAAVTK--YKQNGMSHKDLRLSLHLK-PSSEGLAIVTKYITKGMKEVH 210
Db      246  IANVEDAIKALKPAMVKIARQNMK-----KHMAPKIPNSTLESKILT-----FK 293
Qy      211  ELYEKALSVETEKLLKYLEAVEKVKRTKDELEVH-----LIEHRLYREHLIT 260
Db      294  DLIFCHISEPERKENVYKILG--KKYKTEEBEYKAFGDSASAPFNPBLAGRMKIEIKT 351
Qy      261  --NHUKSK-----EYWKALL--QEMPLTALLNLGKMTANSVLEPNSSEV--SLVCEKLCN 310
Db      352  WENELSAAGNTAEVWDNLISSNQLPYMAMLRNL-----SNLIKAGVSDTTHSIVINKICE 406
Qy      311  EKLKKARHPHILIALETY-----KTGHGLRGKL-----KWRPDE 347
Db      407  PRAVENSMPFLQFSPSAIEAVNEAVTKGFKAKGRNNMLKQGLIENVKVEKTEDEKKDM 466
Qy      348  EILKALDAAFYKTFKVEPTGRPL-----LAV-----DVSASMNOR 384
Db      467  ELEQTEEBGEF---VKNVNGIGKQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTS 523
Qy      385  VLGSLINASTVAAMN-----CMVVTREKDSYVV--AFSDENVPCVTTDM----- 428
Db      524  MSGGAKKYGVSRTCECALVIGLWVKORCEKSSFYIFSSPSQCNKCYLEVDLPEDDELRP 583
Qy      429  TLQOVLAMMSQIPAGTDCSLPMI--WAKKNTTPADVPIVFTDNETFAG-----GVHP 479
Db      584  SMOKLQERKGL--GGGTDPPYECIDEMT--KNKTHVDNIVILSDMMIAGYSDINVRGSSI 641

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QY 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP-DDRGMIDMCGFPTGAL----- 527
 Db 642 VNSIKKTKDEVNPNIKIFAVDLEGYGKLMIGDEFENNNYIKIFGMSDILKFIASAKOG 701

QY 528 ----DVIRNFTLDMI 538
 Db 702 ANNVEVIKNFALOKI 716

RESULT 13
 US-08-854-050-7
 ; Sequence 7, Application US/08854050
 ; Patent No. 6261836

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-854-050-7

Query Match 6.5%; Score 180.5; DB 2; Length 719;

Best Local Similarity 20.7%; Pred. No. 3.8e-08;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

QY 102 GSDISITKQAAFKAVSEVCRIFPTLFTFIOFKDLKSKMKGMGRLAKALADVYNKGG 161
 Db 193 CTESQRKTFMYRFLS-----VTKQKMDYTKKREKELTKL--QALSESBSKRETFD 245

QY 162 M-----ALALAVTK--YKQRNGWSHKDLRLSHLK-PSSEGLAVTYITTKMKREH 210
 Db 246 INNVEDAIKALKRAVVKKIAKQNAK-----KHKAKIKINSTLESKYL-----FK 293

QY 211 ELYEKALSVETKLLKYLEAVEKVKRTQDELYIH-----LIEHRLVREHLIT 260
 Db 294 DLIKFCHIISPKERVYKILG--KKYPTREBYKAAGDSASAFNPBLAKRMKIRISKY 351

QY 261 --NHLSK-----EVRKALL--QEMPLTALRLNGKXTANSVLBPNGSEV--SLVCELTGN 310
 Db 352 WENELSAKGTAAVWDLNLISSNQLPYWMLRNL-----SNILKAGVSDTTHSIVINKICE 406

QY 311 EKLKKARIPHPIILALLETY-----KTGHLRGKL-----KWRPDE 347
 Db 407 PKAVENSKMFPPLQFPFSLIENVBAVTKGFKAQKRENNLKGQIENVAVVEKTDDEKKDM 466

QY 348 EILKALDAFYTKFTVETGKRFPL----LAV-----DVSASNNOR 384
 Db 467 ELQTEGGEF---VKVNEGIGQYINSIELAIVANKNLDEIKGHTAIFSDSGSMSTS 523

QY 385 VLGSILNASTVNAAM-----GMVVTREKDSYVV--AFSDEWVPCVPTTDM----- 428
 Db 524 MSGAKKYGSGVTRTCBICALVGLMVKORCEKSSFYIFSSPSQCNKCYLEVLDLFGDELRLP 583

QY 429 TLQOVLMASQIPAGTDCSLPMI--WAQKTNTPADVIFVTNTEPAG-----GVHP 479
 Db 584 SMQKLDQEKKGL--GGGTDPEYECIDEWT--KQKHVNDIVILSDMLABGSDINVRSSSI 641

QY 480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP-DDRGMIDMCGFPTGAL----- 527
 Db 642 VNSIKKTKDEVNPNIKIFAVDLEGYGKLMIGDEFENNNYIKIFGMSDILKFIASAKOG 701

QY 528 ----DVIRNFTLDMI 538
 Db 702 ANNVEVIKNFALOKI 716

RESULT 14
 US-09-430-323-7
 ; Sequence 7, Application US/09430323
 ; Patent No. 6309867

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6309867el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,323
 FILING DATE: 29-Oct-1999

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 719 amino acids
    TYPE: amino acid
    STRANDNESS: not relevant
    TOPOLOGY: not relevant
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-323-7

Query Match      6.5% Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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RESULT 15
US-09-402-181B-219
  Sequence 219, Application US/09402181B
  Patent No. 6610839
  GENERAL INFORMATION:
    APPLICANT: Cech, Thomas R.
    Lingner, Joachim
    Nakamura, Toru
    Chapman, Karen B.
    Morin, Gregg B.
    Harley, Calvin B.
    Andrews, William H.
  TITLE OF INVENTION: Human Telomerase Catalytic Subunit
  NUMBER OF SEQUENCES: 633
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/402,181B
    FILING DATE: 29-Sep-1997
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/911,312
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/912,951
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/915,503
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: WO PCT/US97/17885
    FILING DATE: 01-OCT-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Ausubius, Scott L.
    REGISTRATION NUMBER: 42,271
    REFERENCE/DOCKET NUMBER: 015389-002620US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 219:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 719 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 219:
US-09-402-181B-219

Query Match      6.5% Score 180.5; DB 2; Length 719;
Best Local Similarity 20.7%; Pred. No. 3.8e-08;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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OM protein - protein search, using SW model

Run on: January 13, 2006, 11:10:45 ; Search time 116 Seconds
(without alignments)
1937.864 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
Sequence: 1 MESSVNQMPLEKQIANSQ.....MCGPDTGALDIVRNFTLDMT 538

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2787	100.0	538	4	US-10-615-515-6 Sequence 6, App1
2	2787	100.0	538	4	US-10-788-792-196 Sequence 196, App
3	2787	100.0	552	4	US-10-288-858-1 Sequence 1, App1
4	2782	99.8	553	4	US-10-288-858-2 Sequence 2, App1
5	2782	99.8	553	4	US-10-288-858-6 Sequence 6, App1
6	2522.5	90.5	537	4	US-10-615-515-10 Sequence 10, App1
7	2269	81.4	538	4	US-10-615-515-11 Sequence 11, App1
8	1011	36.3	643	4	US-10-615-515-12 Sequence 12, App1
9	185.5	6.7	641	6	US-11-097-143-5949 Sequence 5949, Ap
10	180.5	6.5	699	3	US-09-843-676-52 Sequence 52, App1
11	180.5	6.5	699	3	US-09-766-253-52 Sequence 52, App1
12	180.5	6.5	699	3	US-09-438-486-52 Sequence 52, App1
13	180.5	6.5	699	4	US-10-053-758-52 Sequence 52, App1
14	180.5	6.5	699	4	US-10-054-295-52 Sequence 52, App1
15	180.5	6.5	699	4	US-10-054-611-52 Sequence 52, App1
16	180.5	6.5	699	4	US-10-325-810-188 Sequence 188, App
17	180.5	6.5	699	5	US-10-877-124-188 Sequence 188, App
18	180.5	6.5	699	5	US-10-877-022-188 Sequence 188, App
19	180.5	6.5	699	5	US-10-877-146-188 Sequence 188, App
20	180.5	6.5	719	3	US-09-843-676-7 Sequence 7, App1
21	180.5	6.5	719	3	US-09-766-253-7 Sequence 7, App1
22	180.5	6.5	719	3	US-09-438-486-7 Sequence 7, App1
23	180.5	6.5	719	4	US-10-053-758-7 Sequence 7, App1
24	180.5	6.5	719	4	US-10-054-295-7 Sequence 7, App1
25	180.5	6.5	719	4	US-10-054-611-7 Sequence 7, App1
26	180.5	6.5	719	4	US-10-325-810-219 Sequence 219, App
27	180.5	6.5	719	5	US-10-877-124-219 Sequence 219, App

28	180.5	6.5	719	5	US-10-877-022-219 Sequence 219, App
29	180.5	6.5	719	5	US-10-877-146-219 Sequence 219, App
30	130.5	4.7	1937	5	US-10-723-860-58 Sequence 58, App1
31	130.5	4.7	1937	5	US-10-723-860-106 Sequence 106, App
32	123	4.4	23	4	US-10-376-121A-48 Sequence 48, App1
33	120.5	4.3	720	4	US-10-437-963-167109 Sequence 167109, A
34	120	4.3	824	4	US-10-108-260A-4573 Sequence 4573, Ap
35	120	4.3	892	4	US-10-205-219-102 Sequence 102, App
36	119.5	4.3	876	5	US-10-723-860-60 Sequence 60, App1
37	116	4.2	22	4	US-10-376-121A-55 Sequence 55, App1
38	116	4.2	1177	5	US-10-732-923-3293 Sequence 3293, Ap
39	115.5	4.1	550	4	US-10-104-047-3495 Sequence 3495, App
40	115.5	4.1	571	4	US-10-282-122A-77167 Sequence 77167, A
41	115	4.1	561	3	US-09-895-913A-334 Sequence 334, App
42	114.5	4.1	1128	5	US-10-732-923-3317 Sequence 3317, Ap
43	114.5	4.1	1418	4	US-10-365-483-22315 Sequence 22315, A
44	113.5	4.1	2025	4	US-10-788-792-180 Sequence 180, App
45	113	4.1	1577	4	US-10-365-493-6924 Sequence 6924, Ap

ALIGNMENTS

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RESULT 1
US-10-615-515-6
; Sequence 6, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: FAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 538
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-615-515-6

Query Match      100.0%; Score 2787; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-243;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MESSVNQMPLEKQIANSQDGYVQVDMNRLHFLCGSEGGTYIYKQKLGLENAA 60
DB      1 MESSVNQMPLEKQIANSQDGYVQVDMNRLHFLCGSEGGTYIYKQKLGLENAA 60

QY      61 LIRLIEDGRCGVIOEIKSFQSEGGTYOEPMLFALICQSCSDISTQAAKRAVSEVCR 120
DB      61 LIRLIEDGRCGVIOEIKSFQSEGGTYOEPMLFALICQSCSDISTQAAKRAVSEVCR 120

QY      121 IPTHLETFIOFKODKESKCGMGRALRKALADYVNEKGNALALAVTKYKORNGWSHK 180
DB      121 IPTHLETFIOFKODKESKCGMGRALRKALADYVNEKGNALALAVTKYKORNGWSHK 180

QY      181 DILRLSHLKPSSSEGLAVTKYITKGKVEVHELKYEKALSVETBKILKYIAEVKRYKTD 240
DB      181 DILRLSHLKPSSSEGLAVTKYITKGKVEVHELKYEKALSVETBKILKYIAEVKRYKTD 240

QY      241 ELSEVHLIEKHLVREHLLTNHLKSKYWKALLOMPRLALRNIGKMPANSVLEBGNSE 300
DB      241 ELSEVHLIEKHLVREHLLTNHLKSKYWKALLOMPRLALRNIGKMPANSVLEBGNSE 300

QY      301 VSLVEKICNEKLLKKARLHPHILIALETYKYGRLRGLKMRPDEBITKALDAFYK 360
DB      301 VSLVEKICNEKLLKKARLHPHILIALETYKYGRLRGLKMRPDEBITKALDAFYK 360
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Db 301 VSLVCEKLCNEKLLKKARIRHPHILALLETYKTGHLRGKLRKWRPDEIILKALDAAFYKT 360
 Qy 361 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 420
 Db 361 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 420
 Qy 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIAQKNTNPADVIVFTDNETFAGGVHFA 480
 Db 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIAQKNTNPADVIVFTDNETFAGGVHFA 480
 Qy 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 538
 Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 538

RESULT 2

US-10-788-792-196
 ; Sequence 196, Application US/10788792
 ; Publication No. US20040191819A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Pharmaceuticals Corporation
 ; APPLICANT: Eveleigh, Deepa
 ; APPLICANT: Bigwood, Douglas
 ; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
 ; FILE REFERENCE: 5152
 ; CURRENT APPLICATION NUMBER: US/10/788,792
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIOR APPLICATION NUMBER: US 60/450,655
 ; PRIOR FILING DATE: 2003-02-28
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 196
 ; LENGTH: 538
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-788-792-196

Query Match 100.0%; Score 2787; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 2.4e-243;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSVNMQPLNEKQIANSQDGYVQVTDNRRLHFLCFSGEGTYYIKQKGLLENABA 60
 Db 1 MESSVNMQPLNEKQIANSQDGYVQVTDNRRLHFLCFSGEGTYYIKQKGLLENABA 60
 Qy 61 LIRLIEGRGCEVYQETKSFQSGRTTKQBPMLPALAICQCCSDISTKQAAFVSEVCR 120
 Db 61 LIRLIEGRGCEVYQETKSFQSGRTTKQBPMLPALAICQCCSDISTKQAAFVSEVCR 120
 Qy 121 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 180
 Db 121 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 180
 Qy 181 DLRLSHLKPSSGLAVTKYITTKGKEVHLYEKKALSVETEKLLKYLEAVEKVKTKD 240
 Db 181 DLRLSHLKPSSGLAVTKYITTKGKEVHLYEKKALSVETEKLLKYLEAVEKVKTKD 240
 Qy 241 ELAVYHLIEBRLVREHLITNHLKSEVWKLLOEMPLTALLRLNGKRTANSVLEPGNSE 300
 Db 241 ELAVYHLIEBRLVREHLITNHLKSEVWKLLOEMPLTALLRLNGKRTANSVLEPGNSE 300
 Qy 301 VSLVCEKLCNEKLLKKARIRHPHILALLETYKTGHLRGKLRKWRPDEIILKALDAAFYKT 360
 Db 301 VSLVCEKLCNEKLLKKARIRHPHILALLETYKTGHLRGKLRKWRPDEIILKALDAAFYKT 360
 Qy 361 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 420
 Db 361 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 420
 Qy 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIAQKNTNPADVIVFTDNETFAGGVHFA 480
 Db 421 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIAQKNTNPADVIVFTDNETFAGGVHFA 480

Qy 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 538
 Db 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 538

RESULT 3

US-10-288-858-1
 ; Sequence 1, Application US/10288858
 ; Publication No. US20030109001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burchardt, Jean
 ; APPLICANT: Haas, Michael
 ; APPLICANT: Lehmann, Hans-Peter
 ; TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins
 ; FILE REFERENCE: RDID 0052US
 ; CURRENT APPLICATION NUMBER: US/10/288,858
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: DE 19931380.6
 ; PRIOR FILING DATE: 1999-07-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 552
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: SSAG6 M4-C6
 ; US-10-288-858-1

Query Match 100.0%; Score 2787; DB 4; Length 552;
 Best Local Similarity 100.0%; Pred. No. 2.5e-243;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSVNMQPLNEKQIANSQDGYVQVTDNRRLHFLCFSGEGTYYIKQKGLLENABA 60
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 Qy 61 LIRLIEGRGCEVYQETKSFQSGRTTKQBPMLPALAICQCCSDISTKQAAFVSEVCR 120
 Db 73 LIRLIEGRGCEVYQETKSFQSGRTTKQBPMLPALAICQCCSDISTKQAAFVSEVCR 132
 Qy 121 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 180
 Db 133 IPTHLFTFIQPKDKESMKCGMGRALRAKAIADWYNEKGMALALAVTKYKORNGSHK 192
 Qy 181 DLRLSHLKPSSGLAVTKYITTKGKEVHLYEKKALSVETEKLLKYLEAVEKVKTKD 240
 Db 193 DLRLSHLKPSSGLAVTKYITTKGKEVHLYEKKALSVETEKLLKYLEAVEKVKTKD 252
 Qy 241 ELAVYHLIEBRLVREHLITNHLKSEVWKLLOEMPLTALLRLNGKRTANSVLEPGNSE 300
 Db 253 ELAVYHLIEBRLVREHLITNHLKSEVWKLLOEMPLTALLRLNGKRTANSVLEPGNSE 312
 Qy 301 VSLVCEKLCNEKLLKKARIRHPHILALLETYKTGHLRGKLRKWRPDEIILKALDAAFYKT 360
 Db 313 VSLVCEKLCNEKLLKKARIRHPHILALLETYKTGHLRGKLRKWRPDEIILKALDAAFYKT 372
 Qy 361 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 420
 Db 373 PKTVEPTGKRLAVDVASASNNQVLSIINASTVAAAMCMVTRTERKDSYVAFSDMV 432
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 Db 433 PCPVTMTLQOVVMAASQIPAGGTDGSLPMIAQKNTNPADVIVFTDNETFAGGVHFA 492
 Qy 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 538
 Db 493 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDMI 550

RESULT 4

US-10-288-858-2

Sequence 2, Application US/10288858
 Publication No. US20030109001A1
 GENERAL INFORMATION:
 APPLICANT: Burchardt, Jean
 APPLICANT: Haase, Michael
 APPLICANT: Lehmann, Hans-Peter
 TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins
 FILE REFERENCE: RDID 005205
 CURRENT APPLICATION NUMBER: US/10/288,858
 CURRENT FILING DATE: 2002-11-06
 PRIOR APPLICATION NUMBER: DE 19931380.6
 PRIOR FILING DATE: 1999-07-07
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 553
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: SSA60 M56
 US-10-288-858-2

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 7,1e-243; Indels 0; Gaps 0;
 Matches 537; Conservative 0; Mismatches 0;

QY 2 EESVQMPLEKQIANSODGYVQVTDNRLHRLCFSEGGTYIYKEQKLGLENAL 61
 DB 17 EESVQMPLEKQIANSODGYVQVTDNRLHRLCFSEGGTYIYKEQKLGLENAL 76
 QY 62 IRLIEDGCEVIQIKSFQSGRTTKQEPMLPALAICSCSDISTKQAAFAVSEVCRI 121
 DB 77 IRLIEDGCEVIQIKSFQSGRTTKQEPMLPALAICSCSDISTKQAAFAVSEVCRI 136
 QY 122 PTHLFTPIQPKDKESMKCGMGRALRAIADWNEKGMAALAAVTKYKORNGSHD 181
 DB 137 PTHLFTPIQPKDKESMKCGMGRALRAIADWNEKGMAALAAVTKYKORNGSHD 196
 QY 192 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 241
 DB 197 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 256
 QY 242 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSYLEGNSV 301
 DB 257 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSYLEGNSV 316
 QY 302 SLVCEKLCNEKILKARHHPHILIALETTYKTHGRLGRLKMRPDEILKALDAAFYKTF 361
 DB 317 SLVCEKLCNEKILKARHHPHILIALETTYKTHGRLGRLKMRPDEILKALDAAFYKTF 376
 QY 362 KTVPEPTGRFLAADVSAAMQVLSILNASTVAAACMVVTRTEKDSYVAFSDENVP 421
 DB 377 KTVPEPTGRFLAADVSAAMQVLSILNASTVAAACMVVTRTEKDSYVAFSDENVP 436
 QY 422 CVTTDMTLQOVLAMASQIPAGTDCSLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 481
 DB 437 CVTTDMTLQOVLAMASQIPAGTDCSLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 496
 QY 482 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIARNFTLDMI 538
 DB 497 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIARNFTLDMI 553

RESULT 5
 US-10-288-858-6
 Sequence 6, Application US/10288858
 Publication No. US20030109001A1
 GENERAL INFORMATION:
 APPLICANT: Burchardt, Jean
 APPLICANT: Haase, Michael
 APPLICANT: Lehmann, Hans-Peter
 TITLE OF INVENTION: Process for the Recombinant Production of Ribonucleoproteins

FILE REFERENCE: RDID 005205
 CURRENT APPLICATION NUMBER: US/10/288,858
 CURRENT FILING DATE: 2002-11-06
 PRIOR APPLICATION NUMBER: DE 19931380.6
 PRIOR FILING DATE: 1999-07-07
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 6
 LENGTH: 553
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-288-858-6

Query Match 99.8%; Score 2782; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred. No. 7,1e-243; Indels 0; Gaps 0;
 Matches 537; Conservative 0; Mismatches 0;

QY 2 EESVQMPLEKQIANSODGYVQVTDNRLHRLCFSEGGTYIYKEQKLGLENAL 61
 DB 17 EESVQMPLEKQIANSODGYVQVTDNRLHRLCFSEGGTYIYKEQKLGLENAL 76
 QY 62 IRLIEDGCEVIQIKSFQSGRTTKQEPMLPALAICSCSDISTKQAAFAVSEVCRI 121
 DB 77 IRLIEDGCEVIQIKSFQSGRTTKQEPMLPALAICSCSDISTKQAAFAVSEVCRI 136
 QY 122 PTHLFTPIQPKDKESMKCGMGRALRAIADWNEKGMAALAAVTKYKORNGSHD 181
 DB 137 PTHLFTPIQPKDKESMKCGMGRALRAIADWNEKGMAALAAVTKYKORNGSHD 196
 QY 192 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 241
 DB 197 LRLSHLKPSSEGLAVTKYITKGMEVHELYKEKALSVETEKLYLEAVEKVKRTQDE 256
 QY 242 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSYLEGNSV 301
 DB 257 LEVHILIEBHRLVREHLITNHLKSKVWKALLOEMPLTALLNLGKMTANSYLEGNSV 316
 QY 302 SLVCEKLCNEKILKARHHPHILIALETTYKTHGRLGRLKMRPDEILKALDAAFYKTF 361
 DB 317 SLVCEKLCNEKILKARHHPHILIALETTYKTHGRLGRLKMRPDEILKALDAAFYKTF 376
 QY 362 KTVPEPTGRFLAADVSAAMQVLSILNASTVAAACMVVTRTEKDSYVAFSDENVP 421
 DB 377 KTVPEPTGRFLAADVSAAMQVLSILNASTVAAACMVVTRTEKDSYVAFSDENVP 436
 QY 422 CVTTDMTLQOVLAMASQIPAGTDCSLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 481
 DB 437 CVTTDMTLQOVLAMASQIPAGTDCSLPMIWAQKNTNPADVFIYFTDNETPAGGVHPAI 496
 QY 482 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIARNFTLDMI 538
 DB 497 ALREYRKQMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGPDTGALDVIARNFTLDMI 553

RESULT 6
 US-10-615-515-10
 Sequence 10, Application US/10615515
 Publication No. US20040132974A1
 GENERAL INFORMATION:
 APPLICANT: PAGAN, RICHARD, JOSEPH
 APPLICANT: GUTTERIDGE, ALEX
 APPLICANT: CHRISTOPHER BENJAMIN
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-2004
 CURRENT APPLICATION NUMBER: US/10/615,515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: GB 0100750.9
 PRIOR FILING DATE: 2001-01-11
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 10

LENGTH: 537
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-615-515-10

Query Match 90.5%; Score 2522.5; DB 4; Length 537;
 Best Local Similarity 89.8%; Pred. No. 2.3e-219;
 Matches 483; Conservative 28; Mismatches 26; Indels 1; Gaps 1;

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QY 1 MESSVNOQPIANEKOIANSODGYVQVTDNRRHLRFLCFSEGGTYYIKKQKGLNENAEA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEGSANOLOPSESTQVNVSEGGCWQVTDNQ-VRRFLCFSEGGTYYIKKQKGLNENAEA 59
QY 61 LIRLIDEGRCGEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 LIRLIDEGRCGEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 119
QY 121 IPTHLFTPIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 IPTHLFTPIQPKDKLKSMMCGMGRALRKAVADWYNEKGMALALAVTKYKQKNGSHK 179
QY 181 DLRLSHLKPSSEGLAIVTKYITGKMGVHELYEKAISVTEKGLKYLEAVEKVKTKD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 DLRLSHLKPSSEGLAIVTKYITGKMGVHELYEKAISVTEKGLKYLEAVEKVKTKD 239
QY 241 ELEVIHLIEHRILVREHLITNHLKSKEWKALLOEMPLTALLRNLGKWTANSVLEPNS 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 DLEVIHLIEHQVREHLITNHLKSKEWKALLOEMPLTALLRNLGKWTANSVLEPNS 299
QY 301 VSLVCEKLCNEKLIKARIPHPHILIALETYKTHGHLGKLRPDEEILKALDAAFYKT 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 VSLVCEKLSNEKLIKARIPHPHILIALETYKTHGHLGKLRPDKOILQALDAAFYTT 359
QY 361 FKTYEPTGRKFLAVDVASAMNORVLGSIINASTVAAMCNAVTRTEKDSVVAFSDENV 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 FKTYEPTGRKFLAVDVASAMNORVLGSIINASTVAAMCNAVTRTEKDSVVAFACDMV 419
QY 421 PCPTVTMTLOOVLVAMNSQIPAGGTDCLPMIWAOKNTPADVIVFTDNETPAGVHPA 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 PCPTVTMTLOOVLVAMNSQIPAGGTDCLPMIWAOKNTPADVIVFTDNETPAGVHPA 479
QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 480 VALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 537

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RESULT 7
 US-10-615-515-11
 Sequence 11, Application US/10615515
 Publication No. US20040132974A1
 GENERAL INFORMATION:
 APPLICANT: PAGAN, RICHARD, JOSEPH
 APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
 APPLICANT: GUTTERIDGE, ALEX
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-2004
 CURRENT APPLICATION NUMBER: US/10/615, 515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: GB 0100750.9
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 11
 LENGTH: 538
 TYPE: PRT
 ORGANISM: Xenopus laevis
 US-10-615-515-11

Query Match 81.4%; Score 2269; DB 4; Length 538;
 Best Local Similarity 78.6%; Pred. No. 2.2e-196;
 Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;

```

QY 1 MESSVNOQPIANEKOIANSODGYVQVTDNRRHLRFLCFSEGGTYYIKKQKGLNENAEA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEATMDQTPLANEKQVNPSEGCYVQVSDNNRLRFLCFSEGGTYYIKKQKGLNENAEA 60
QY 61 LIRLIDEGRCGEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LIRLIDEGRCGEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQAFKAVSEVCR 120
QY 121 IPTHLFTPIQPKDKLKSMMCGMGRALRKAIADWYNEKGMALALAVTKYKQKNGSHK 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 IPTHLFTPIQPKDKLKSMMCGMGRALRKAVADWYNEKGMALALAVTKYKQKNGSHK 180
QY 181 DLRLSHLKPSSEGLAIVTKYITGKMGVHELYEKAISVTEKGLKYLEAVEKVKTKD 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 DLRLSHLKPSSEGLAIVTKYITGKMGVHELYEKAISVTEKGLKYLEAVEKVKTKD 240
QY 241 ELEVIHLIEHRILVREHLITNHLKSKEWKALLOEMPLTALLRNLGKWTANSVLEPNS 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 ELEVIHLIEHRILVREHLITNHLKSKEWKALLOEMPLTALLRNLGKWTANSVLEPNS 300
QY 301 VSLVCEKLCNEKLIKARIPHPHILIALETYKTHGHLGKLRPDEEILKALDAAFYKT 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 VSSVCEKLTNEKLIKARIPHPHILIALETYKTHGHLGKLRPDKOILQALDAAFYKS 360
QY 361 FKTYEPTGRKFLAVDVASAMNORVLGSIINASTVAAMCNAVTRTEKDSVVAFSDENV 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 FKTYEPTGRKFLAVDVASAMNORVLGSIINASTVAAMCNAVTRTEKDSVVAFSDENV 420
QY 421 PCPTVTMTLOOVLVAMNSQIPAGGTDCLPMIWAOKNTPADVIVFTDNETPAGVHPA 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 PCPTVTMTLHEVEYKSDITMGSTDCALPMIWAOKNTPADVIVFTDNETPAGVHPA 480
QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 481 TALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDGALDVIRNFTLDM 538

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RESULT 8
 US-10-615-515-12
 Sequence 12, Application US/10615515
 Publication No. US20040132974A1
 GENERAL INFORMATION:
 APPLICANT: PAGAN, RICHARD, JOSEPH
 APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
 APPLICANT: GUTTERIDGE, ALEX
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-2004
 CURRENT APPLICATION NUMBER: US/10/615, 515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: GB 0100750.9
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 12
 LENGTH: 643
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-10-615-515-12

Query Match 36.3%; Score 1011; DB 4; Length 643;
 Best Local Similarity 36.3%; Pred. No. 3.1e-82;
 Matches 215; Conservative 111; Mismatches 204; Indels 62; Gaps 9;

```

QY 7 OMOPINEKOIANSODGYVQVTDNRRHLRFLCFSEGGTYYIKKQKGLNENAEA 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 54 OMEKYKQGVENNAAGVFPVSDTYQVRRFLIGSDKSHQSEKTIIDNAQRIKITE 113
QY 67 DGRGCEVIOEIKSFQSGRTTKQEPMLPALAICSCQSDISTKQ----- 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 114 QGNHMYLKEIALINAEINRNPKNAMITFLAICARISTHDTTKTECPMLNAYSDYRAL 173

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110 --AAFKAVSEVCRIPHTLFTFIOFKDLKESMKG-----MGRALKKAIADYNEKG 161
 174 HDSALDLIPVCRFTPLFFBFDVYQOTISESTKAGAKSSTGWSMNAISKWTTKTT 233
 162 MALAAVTKYQORNGMSHKDLRLSH---LKPSSGLA-----IYKITYTKG----- 205
 234 EKLMLTKYQORNGMSHKDLRLSH---LKPSSGLA-----IYKITYTKG----- 205
 206 -----WKEVHELKKEKALSY-----ETKLLKYLEAVKVKRTKDELEVIHLI 248
 294 RKMSEVSEAEVKEKDKALKLPYEBOLIKESGRALNVAIYAKLNEGSEVIVAAI 353
 249 ESHRLVREHLITNHLKSEVWKALIQ-EMPLTALLRNIGKMTANSVLEPGNSEVSLVCEK 307
 354 KKHGVRRHLPTTSLNSKLWVETLFDVSGPMTAMIRNLAKTIVGALD--EKRVNIVR 411
 308 LCNKGLKKARIPHHILALETTKYGKGLKMKRPDEILKALDAFYKTEKTEPT 367
 412 LTDOELRRSRHPIINLTPARAVYAQGRDGKSLTWEPQKICDLEAGFYAFVNAAPT 471
 368 GKRPLAVDVASAMQORVGSITNASVAAACMVVTRTEKDSYVAFSDEWPCPTTD 427
 472 GGRVCLADVSGMSTRVSSPISCREAKYKMSLINLNEAEVRCVACDKLTLPFTKD 531
 428 MTLQOVLMAMSOIPAGTDCSLPMIWAOKTNPADVFTVFTDNETFAGGVHDAALREYR 487
 532 WKIGVNVYNNLDGRDTCGLPMTWATENNLPKPVFIITYDNDTWAGIHPEPAIKKR 591
 488 KKMID-PAKLIVCGMTSNGFTIADPDGRGMLDMCGEPDGLADVIRNFIIDMI 538
 592 EASGHDHAKVIVMAQAYDYSIADPSDAGMLDITGDSAVQIVHIEFVTGKI 643

RESULT 9
 US-11-097-143-5949
 / Sequence 5949, Application US/11097143
 / Publication No. US20050208558A1
 / GENERAL INFORMATION:
 / APPLICANT: Venter, J. Craig
 / APPLICANT: et al.
 / TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 / TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 / FILE REFERENCE: CLO00728
 / CURRENT APPLICATION NUMBER: US/11/097,143
 / CURRENT FILING DATE: 2005-04-04
 / PRIOR APPLICATION NUMBER: 60/157,832
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: 60/160,191
 / PRIOR FILING DATE: 1999-10-19
 / PRIOR APPLICATION NUMBER: 60/161,932
 / PRIOR FILING DATE: 1999-10-28
 / PRIOR APPLICATION NUMBER: 60/164,769
 / PRIOR FILING DATE: 1999-11-12
 / PRIOR APPLICATION NUMBER: 60/173,383
 / PRIOR FILING DATE: 1999-12-28
 / PRIOR APPLICATION NUMBER: 60/175,693
 / PRIOR FILING DATE: 2000-01-12
 / PRIOR APPLICATION NUMBER: 60/184,831
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: 60/191,637
 / PRIOR FILING DATE: 2000-03-23
 / NUMBER OF SEQ ID NOS: 43008
 / SOFTWARE: Pabseq for Windows Version 4.0
 / SEQ ID NO: 5949
 / LENGTH: 641
 / TYPE: PR
 / ORGANISM: DROSOPHILA
 / US-11-097-143-5949

Query Match 6.7%; Score 185.5; DB 6; Length 641;
 Best Local Similarity 19.5%; Pred. No. 2.1e-07;

Matches 123; Conservative 108; Mismatches 242; Indels 159; Gaps 28;
 1 MESSVNOQOPANE---KOIANSQOG-YVQVOTDNKRLHRLFCPS-BGGTYIIEQKGL 55
 64 MEKKAISNQPKDPSKDEPQOSGTALSTIPALDKRRFCISTDEPVTTPALDLV 123
 56 EN-----AEALIRLIEDPGEVIOEIKSF-----SQGRITKQEPMLFALAIQSQSDI 105
 124 ENNPAASLKELOSVSEDE---ELVECLISVUGSEPNQPRPRPEBLLIILVFTTCDE 179
 106 STKQAAFKAVSEVCRIPHTLFTFIOFKDLKESM-KCGMGRALKKAIADYNEKGVAL 164
 180 KKRNAVRRPFDLTSSDILLFQVYKRGKLEKTPFRFTRKAVIANYGFK-SIDR 238
 165 ALAVTKYQORNGM-SHKDLRLSHKRS--EGLAIVKITYTKGKVNHE-----L 212
 239 LIHFWISIGDGRWPAHRDLRLYLRHFRANFLPEIILALRLSSSPKELSQWPDFTPLTS 298
 213 YKKAISVETKELKYLE-AVEKVKRTKDELEVI--HLIEHRLVREHLITNHLKSEVW 269
 299 FRETIQGVKRLTLDEPQALSYKGLSLSWEHVPFHLHPRLA--HFLIPMS-----Y 352
 270 KALIQEMPLTALLRNIGKMTANSVLEPGNSEVSLVCEKLCNEKGLKKARIPHHILALE 329
 353 EQLQKMPRLSRL-----NSRVRRPABQLDKCKKASNVPPVRLLE-- 395
 330 TYKYGHLRGKLMRPDEILKAL-----DAAFYK-----TFK 362
 396 -----DMRLRKPKNVQNLVPSLKNKNTFKQCATITSQKASFLHSYVEISFG 445
 353 TVEPTGKFLAVDVASAMQORVGSITNAS-----TVAAACMVVTRTEKDSYVAF 415
 446 LNKALGR--LHTTLLEQAVYLGKYLSPGCRSLKYDALVALFGYFRSPKRYTVERW 501
 416 SD---EMVPCPVYTDMTLQOVLMAMSOIPAGTDCSLPMIWAOKTNT----- 459
 502 HDRSGKALAPMTNMSVSE-----AKTCB-----NQKNTPHNRSPTVIDLR 546
 460 -----PADVFTVFTDNETFAGGVH-----AIAKRYRKMDIPALIVCGM-- 501
 547 PRALDMQNTFDFVFLVAVG--AARGNPENNSKCLALMLDKYRKRNSNAFIVSLQ 603
 502 TSNGFTIADPDGRGMLDMCGEPDGLADVIRNFIIDMI 538
 604 RQRSMIYSSGRNENLELCSLDKHTPRLINAF 635

RESULT 10
 US-09-843-676-52
 / Sequence 52, Application US/09843676
 / Patent No. US20020164786A1
 / GENERAL INFORMATION:
 / APPLICANT: Cech, Thomas R.
 / Lingner, Joachim
 / Nakamura, Toru
 / Chapman, Karen B.
 / Morin, Gregg B.
 / Harley, Calvin
 / Andrews, William H.
 / TITLE OF INVENTION: No. US20020164786A1 Telomerase
 / NUMBER OF SEQUENCES: 225
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Townsend and Townsend and Crew LLP
 / STREET: Two Embarcadero Center, 8th Floor
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: United States of America
 / ZIP: 94111
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30


```

NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-053-758-52

Query Match          6.5%; Score 180.5; DB 4; Length 699;
Best Local Similarity 20.7%; Pred.No. 6.7e-07;
Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29

QY 102 CSDISTKQAAPKAAVSEVCRIPTHLTPILOPKDKESMKCGMGALRAKAIADWYNKEG 161
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 175 CTESGRKKTMTRYLS-----VTNRQKKNQOTKKRRKENLITKL--QAIKSEDSKRRTD 227
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 162 M-----ALALAATK--VKQRNGMSHKDLRLSHLK-PSSSGLAIVTKYTITKGKVEH 210
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 228 IAWVEDAIAKAKPAVMKKIAGQNAMK-----KHMKAPKIPNSTLESKYLT-----FK 275
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 211 ELAYEKALSVETBEKLYLEAVEXKYRTQDELEVH-----LIENHLVREHLLT 260
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 276 DLIRFGCHISBPERRYKITLG--KKTPKTBEEIKAAPGDSASAPFPDELAKGMKIPIST 333
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 261 --NHLKSK---EWKALL--QEMFLTLRLNGKTANSVLDPGNSEV--SLVCEKLCN 310
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 334 WENLSAAGNTAEAVWDNLISSQLPYMAWLRL-----SNLMKAGVDTHSIVINKICE 388
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 311 EKLTKARAIHPHILALETY-----KTHGLRGCL-----KKRPB 347
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 389 PKAVENSRTGFLOPFSIAEVAWEAVTGFKAKKRRENMLKQIEAVEVEVEKTEDECKDM 448
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 348 EILVALDAAPKTFPTVEPTGRPL-----LAV-----DVSAQMOR 384
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 449 ELEOTEBSGP--VKVNEIGIQYINSLIELAKIVANKULDEIKGHITALPSDVSGSMSTS 505

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QY      385 YIGSILNASTVAAA-----CWVTEBKOSYV--AFSDEWVPCPVTTD-----428
Db      506 MSGGAKKYSVATTCLECALVIGLWVKQRCESSSYIFSSPSQCKCYLBYVDLPGLDLRP 565S
QY      429 TLQGVLMANSSQIPAGTDCSLPMI--MAQKTNTPADVFYFTNETFAG-----GVHP 479P
Db      566 SMQKLLQEGKGL--GGGTDFPEYCEIDEMT--KQKTHVDNIIVILSDMMIAGVSADINVRGSSI 623S
QY      480 AIAAREYRKQMDIIPAKLVICGNTSNG--FTIADP--DGRGMLDMGFPPTGAL-----527P
Db      624 VNSIKKTKQEVNPNIKIFAVNDLEGYKCLNLGDEPENNVIKIFGMSDSILKFIASAQGG 683S
QY      528 ----DIVRNPFLDMI 538
Db      684 ANNVEYIKKPFALQKI 698

RESULT 14
US-10-054-295-52
; Sequence 52, Application US/10054295
; Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin
            Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 06/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 06/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-054-295-52

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Query Match 6.5%; Score 180.5; DB 4; Length 699;
 Best Local Similarity 20.7%; Pred. No. 6.7e-07;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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102 CSDISTKQAFKAVSEVCRIPHLFTPIQFKDKLSEKMGKMGALKAIDWYNEKGG 161
175 CTESQKKTMYRYS-----VTNKKMDQTKKRRKENLITKL--QAIKSEBKSRETD 227
162 M-----ALAAVTK--YKQRNGMSKDLRLSHLK-PSSEGLAIVTKYITKGMKEVH 210
228 INNVDAIKALPRAVKKIARQNMK-----KMKAPKIPNSTLESKYLT-----FK 275
211 BLYEKALSVETEKLLKYLEAVEKRYKTDELEVH-----LIEHRLVBEHLIT 260
276 DLKFCHESEPEREYKILG--KTKPTEBEYKAAFQGSASAPFNPBLAGKMKIEISKT 333
261 --NHLKSK---EYWKALL--QEMPLTALLRNIGKMTANSVLEPQNSV--SLVCEKLCN 310
334 WENELSAKGNLAEVNDNLISNQLPYMAMLRNL-----SNILKAGVSDTTHSIVINKICE 388
311 EKLKKARIHPHILIALETY-----KTGHGRLGKL-----KMRPDE 347
369 PRAVENSXKFPLOFSAIEAVNEAVTKGFKAKKRENNMLKGQIBAVKEVEKTDDEKDM 448
348 EILKALDAAFYKTFKVEPTGKRF--LAV-----DVSASMNOR 384
449 ELEQTEEGEF--VKYNEGIGKQYINSIELAKIVNKNLDEIKGHTALFSDVSGSMSTS 505
365 VLGSLNSTVAAM-----CMVVTREKDSYVV--AFSDMVPQVPTDM----- 428
506 MSGAKKRGSVRTCECALVLGLMVKORCEKSFYFSSPSQCNKCYLEVLPDDELRLP 565
429 TLOQVLMMSQIPAGTDCSLPMI--MAQKNTVPADVIFVFTDNETFAG-----GVHP 479
566 SMQKLOEGKGL--GGTDPPEYCIBEW--KNTTHVNIYILSDMMAIEGYSDINVRGSSI 623
480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP--DGRGMLMCGFTGAL----- 527
624 VNSIKKYKQEVNPNIKIPAVDLEGYKCLNLGDEFENNYIKIFGMSDSLIFKSAKQGG 683
528 ---DVIRNFTLDMI 538
684 ANNVEVIKNFALOKI 698

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RESULT 15

US-10-054-611-52
 / Sequence 52, Application US/10054611
 / Publication No. US20030059787A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Langner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morlin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 699 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 52:
 US-10-054-611-52

Query Match 6.5%; Score 180.5; DB 4; Length 699;
 Best Local Similarity 20.7%; Pred. No. 6.7e-07;
 Matches 115; Conservative 100; Mismatches 191; Indels 149; Gaps 29;

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102 CSDISTKQAFKAVSEVCRIPHLFTPIQFKDKLSEKMGKMGALKAIDWYNEKGG 161
175 CTESQKKTMYRYS-----VTNKKMDQTKKRRKENLITKL--QAIKSEBKSRETD 227
162 M-----ALAAVTK--YKQRNGMSKDLRLSHLK-PSSEGLAIVTKYITKGMKEVH 210
228 INNVDAIKALPRAVKKIARQNMK-----KMKAPKIPNSTLESKYLT-----FK 275
211 BLYEKALSVETEKLLKYLEAVEKRYKTDELEVH-----LIEHRLVBEHLIT 260
276 DLKFCHESEPEREYKILG--KTKPTEBEYKAAFQGSASAPFNPBLAGKMKIEISKT 333
261 --NHLKSK---EYWKALL--QEMPLTALLRNIGKMTANSVLEPQNSV--SLVCEKLCN 310
334 WENELSAKGNLAEVNDNLISNQLPYMAMLRNL-----SNILKAGVSDTTHSIVINKICE 388
311 EKLKKARIHPHILIALETY-----KTGHGRLGKL-----KMRPDE 347
369 PRAVENSXKFPLOFSAIEAVNEAVTKGFKAKKRENNMLKGQIBAVKEVEKTDDEKDM 448
348 EILKALDAAFYKTFKVEPTGKRF--LAV-----DVSASMNOR 384
449 ELEQTEEGEF--VKYNEGIGKQYINSIELAKIVNKNLDEIKGHTALFSDVSGSMSTS 505
429 TLOQVLMMSQIPAGTDCSLPMI--MAQKNTVPADVIFVFTDNETFAG-----GVHP 479
566 SMQKLOEGKGL--GGTDPPEYCIBEW--KNTTHVNIYILSDMMAIEGYSDINVRGSSI 623
480 AIALREYRKMDIPAKLIVCGMTSNG--FTIADP--DGRGMLMCGFTGAL----- 527
624 VNSIKKYKQEVNPNIKIPAVDLEGYKCLNLGDEFENNYIKIFGMSDSLIFKSAKQGG 683
528 ---DVIRNFTLDMI 538
684 ANNVEVIKNFALOKI 698

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Fri Jan 13 11:44:12 2006

us-10-615-515-6.rapbm

Page 10

Search completed: January 13, 2006, 11:21:45
Job time : 118 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:11:20 ; Search time 31 Seconds
(without alignments)
164.076 Million cell updates/sec

Title: US-10-615-515-6

Perfect score: 2787
Sequence: 1 MESSVNGMQPIKEKQIANSQ.....MCGFDTGALDVIRNFTLDMI 538

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCIT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.5	3.5	596	US-10-453-372-1212	Sequence 1212, Ap
2	98.5	3.5	600	US-10-453-372-1206	Sequence 1206, Ap
3	98.5	3.5	989	US-10-821-234-975	Sequence 975, App
4	98	3.5	2665	US-11-124-368A-214	Sequence 214, App
5	98	3.5	2668	US-11-124-368A-215	Sequence 215, App
6	95.5	3.4	600	US-10-453-372-1204	Sequence 1204, Ap
7	95.5	3.4	819	US-10-453-372-1210	Sequence 1210, Ap
8	95.5	3.4	866	US-11-147-047-32	Sequence 32, Appl
9	95.5	3.4	876	US-10-453-372-1202	Sequence 1202, Ap
10	95.5	3.4	876	US-10-453-372-1208	Sequence 1208, Ap
11	95	3.4	858	US-10-878-555A-113	Sequence 113, App
12	94	3.4	612	US-10-467-657-3988	Sequence 3988, Ap
13	94	3.4	1244	US-11-052-554A-110	Sequence 110, App
14	94	3.4	1404	US-10-878-555A-169	Sequence 169, App
15	93.5	3.4	932	US-11-017-550-65	Sequence 65, Appl
16	92	3.4	512	US-10-467-657-4870	Sequence 4870, Ap
17	91.5	3.3	1266	US-10-995-561-665	Sequence 665, App
18	91.5	3.3	1652	US-10-995-561-663	Sequence 663, App
19	91.5	3.3	1938	US-10-995-561-661	Sequence 661, App
20	91.5	3.3	1938	US-10-995-561-662	Sequence 662, App
21	91.5	3.3	1954	US-10-995-561-660	Sequence 660, App
22	91.5	3.3	1972	US-10-995-561-664	Sequence 664, App
23	91.5	3.3	1972	US-10-995-561-666	Sequence 666, App
24	91.5	3.3	3803	US-10-995-561-773	Sequence 773, App
25	91.5	3.3	3960	US-10-995-561-771	Sequence 771, App

26	91.5	3.3	5335	US-10-995-561-777	Sequence 777, App
27	91.5	3.3	5406	US-10-995-561-774	Sequence 774, App
28	91.5	3.3	5415	US-10-995-561-775	Sequence 775, App
29	91.5	3.3	5464	US-10-995-561-775	Sequence 775, App
30	89.5	3.2	477	US-11-075-185-27	Sequence 27, Appl
31	89.5	3.2	2101	US-10-857-780-23	Sequence 23, Appl
32	89.5	3.2	3056	US-11-109-156-20	Sequence 20, Appl
33	88	3.2	1976	US-11-069-834-54	Sequence 54, Appl
34	87	3.1	557	US-10-467-657-2888	Sequence 2888, Ap
35	87	3.1	1976	US-11-069-834-52	Sequence 52, Appl
36	86	3.1	270	US-10-981-873-47	Sequence 47, Appl
37	86	3.1	491	US-10-793-626-2808	Sequence 2808, Ap
38	85.5	3.1	609	US-10-821-234-1611	Sequence 1611, Ap
39	85.5	3.1	1124	US-11-195-197-9	Sequence 9, Appl1
40	85.5	3.1	1663	US-11-186-284-26	Sequence 26, Appl
41	85.5	3.1	3063	US-11-186-284-26	Sequence 26, Appl
42	85	3.0	3674	US-11-000-463-454	Sequence 454, App
43	84.5	3.0	718	US-10-467-962B-29	Sequence 29, App
44	84.5	3.0	718	US-10-467-962B-65	Sequence 65, Appl
45	84.5	3.0	1377	US-10-467-657-7922	Sequence 7922, Ap

ALIGNMENTS

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RESULT 1
US-10-453-372-1212
; Sequence 1212, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseq1ast version 0.1
; SEQ ID NO 1212
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-453-372-1212

Query Match 3.5%; Score 98.5; DB 6; Length 596;
Best local Similarity 19.0%; Pred. No. 1.6;
Matches 92; Conservative 76; Mismatches 191; Indels 125; Gaps 21;

QY 95 AALAGCGSDISTKQAAFAVSEV-----CRIPHLFTFOFK-----DL 135
Db 5 SVEICNVGCSVEVENLTVNCKEVSYYRPNQKCPWNSNYHNLNPNNTLITLYPNTFLNF 64
QY 136 KESMKCGMGGRRLRLKRLADWYNEKGGMALALAVTKYKQNGNSHKLRLSLKPSSEGL 195
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Db      65 SHAVSLHGNKKLQ-----NIEGAEVLGSLAQHLLNN-NEUKTIRADTF-PGIENTL 115
Oy      196 AI-----YKYITKGMKEVHEIYEKALSVETEKILKYLEAVEKVKYKXODEVILHLE 249
Db      116 EYQADYNYLIKTYERG-AFNKTLHLKVL-LINDLHLSFL-----152
Oy      250 EHRVLEHLLTNHLKSKEVWKALLOEMPTITALLRNIGKMTANSYLE-PGNSEVSLVEKL 308
Db      153 PDNIFPFASIT-HL--DIRGNRIQTLPTIGVLEHIGVLELOEDNPNMNSCDLPLKA 208
Oy      309 CNEKLKKARINHPHLLIALETYKTHGKRGKLRPRBEILKLDAAFYTFKTVPEPTG 368
Db      209 WLENNM-----PYNLYIEBAICETPSPDLYGRL-----LKEYN 239
Oy      369 KREPLAVDVSASNNORVLG-----STLNSVTAAMCMVYTRTEKDSVVAVFDENV 420
Db      240 KOELCPMGCSDPDVAILPSPQLENGYTPPNHITQTSILHRLVTKPPKTTNPSKISG-IV 238
Oy      421 PCFVTTDMTLQOVLAMASQIPAGTDCSLPMIWAOKTNPADVFLVFPTNETPAGVHPA 480
Db      299 AGRALSNRNLSQVLSQTVRVP-LTPCPARPC--KTH-PSDGLGSVNCQEKNIQMSSEL 354
Oy      481 IALREYRKQNDIPAKLIVCGMTSNGETIADPDRGMLDMCEBTDGAL-----DVI 530
Db      355 IPRPLNAKKLHV-----NGNSIKQDVSDPFTPEGIDLHLHGSNQITVIKGDVF 403
Oy      531 RNFT 534
Db      404 HNLT 407

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RESULT 2
US-10-453-372-1206
; Sequence 1206, Application US/10453372
; Publication No. US2006003233A1
; GENERAL INFORMATION:
;   APPLICANT: Alabrook, et al.
;   TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;   FILE REFERENCE: 21402-589 A
;   CURRENT APPLICATION NUMBER: US/10/453,372
;   CURRENT FILING DATE: 2003-06-03
;   PRIOR APPLICATION NUMBER: 09/789390
;   PRIOR FILING DATE: 2001-02-23
;   PRIOR APPLICATION NUMBER: 60/185967
;   PRIOR FILING DATE: 2000-03-01
;   PRIOR APPLICATION NUMBER: 09/623187
;   PRIOR FILING DATE: 2001-03-29
;   PRIOR APPLICATION NUMBER: 60/195792
;   PRIOR FILING DATE: 2000-03-10
;   PRIOR APPLICATION NUMBER: 09/839446
;   PRIOR FILING DATE: 2001-03-19
;   PRIOR APPLICATION NUMBER: 60/199476
;   PRIOR FILING DATE: 2000-03-25
;   PRIOR APPLICATION NUMBER: 09/863776
;   PRIOR FILING DATE: 2001-05-23
;   PRIOR APPLICATION NUMBER: 60/208263
;   PRIOR FILING DATE: 2000-05-31
;   PRIOR APPLICATION NUMBER: 09/939398
;   PRIOR FILING DATE: 2001-08-24
;   PRIOR APPLICATION NUMBER: 60/227800
;   PRIOR FILING DATE: 2000-08-25
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 1609
;   SOFTWARE: Cnaseqblast version 0.1
;   SEQ ID NO 1206
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-453-372-1206

Query Match      3.5%   Score 98.5;   DB 6;   Length 600;
Best Local Similarity  19.0%;   Pred. No. 1.7;

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[illegible]

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RESULT 3
US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US200502551141
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_gene Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975

Query Match      3.5%; Score 98.5; DB 6; Length 989;
Best Local Similarity 20.2%; Pred. No. 3.4;
Matches 67; Conservative 75; Mismatches 114; Indels 75; Gaps 16;

OY      49      KEQKLGIENNAAL-----IRLIED-----GRGCVIOEI--KFSQ 82
          | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
DB      513      KQMLGIIVSPESDMONYSHFHELRLATREBINVLKODLONALBESBRNKEVRLBKLVER 572
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      83      BGRITTKQPM-LFALALCSQSDIS--TKQAF-----KAVSEVCRIPTHLFTPIQK- 132
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      573      EKGIVITKPPVVEVEYEMSSYSLVENNAKKEALFLPEKQEQOEIIMLKQTLIKSGMDQEA 632
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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QY 133 ----KDLKESN-----KCGMGRALRAIDWNEKCGMALALAVTYKQONGMSH 179
 DB 633 SDEADMEKANRMIDELNKOVELSOLYKEAQAELEBYRKRKSLIEDYAEIYHKA--EH 690
 QY 180 KDLRLSLHK--PSESGALATYTKYTKMKWEVHEL-----YKKAUSVEFEBKLLKYLEA 231
 DB 691 EKMQLTIVSPAKADALSEKSOYSKVLNBLTOLKOLVDOKENSVAI-----TERHQV 745
 QY 232 VEKVRRTKOELEVIHLIEBRLVREHLITNHLKSKVKKALLOEMP--LTALLNRLGKMT 289
 DB 746 ITTIRTAKEHE-----EKISNKENHLASKVEVAKLEKQJLEKAAWTDAMVPRSSYEV 800
 QY 290 ANSVLEPNSSEVSLVCEKLCNEKLLKARIRH 320
 DB 801 LOSSLE---SEVSVLASKL--KESVKEKEKVH 827
 RESULT 4
 US-11-124-368A-214
 ; Sequence 214, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CLO01524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214
 ; LENGTH: 2665
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-124-368A-214
 Query Match 3.5%; Score 98; DB 7; Length 2665;
 Best Local Similarity 20.8%; Pred. No. 15;
 Matches 80; Conservative 67; Mismatches 105; Indels 132; Gaps 19;
 QY 49 KEQKGLNENALIRLIDEGCEVIOIKSPSGRTTKQBPMLPALAICSGCSDISTK 108
 DB 1017 KKQDLEAKNTQTLTADVKNBIIIEOQRKIFSLIOEKNELOQ--MLESV-----IAEK 1066
 QY 109 QAAFAVSEVCRIPHLTFPIQFKKDLKESM-----KCGMGRALRK--AIADWYN 157
 DB 1067 E-----OLKTDLKENIEMTIENOBELRLDDELKQOEIYAQEN 1106
 QY 158 ----EKGGWA-----LALAVTYKQ-----RNG 176
 DB 1107 HAIKKEGELSRCDLAEVEELKESQOLQKQOQLNVQEMSEMOKKINEIENLKNB 1166
 QY 177 WSHKDLRLSHLKPSEGLAIVTKYTKMKWEVHELKYKAL-----SVETEK--LKY 228
 DB 1167 LKNKE-LTLEHME--TERLELAQK-LNENYEEVKSITTKERKVLKELQSFETERDLRGY 1222
 QY 229 LEAVKRV-KRTQDELEVIHL-IEBHR-----LVREHLITNHLKSKVW 269
 DB 1223 IREIATGLOTEBELKIAHILKEHOETIDELRVSSEKTAQIINTQDLKSHTKQBEI 1282
 QY 270 KALLQEMPLTALLRNIGKMTANSVLEPGNSVSLVCEKLCNEKLLKARIRHFFHILALE 329
 DB 1283 PVLHEEQ---ELLPNVKEV---SETOETMNELELLTEOSTTKDSTTLARIEM----- 1328
 QY 330 TYKTGHGLRGKLMRPDEEILKAL 353

DB 1329 -----ERLRINEKFOESQOEIKSL 1347
 RESULT 5
 US-11-124-368A-215
 ; Sequence 215, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CLO01524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 215
 ; LENGTH: 2668
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-124-368A-215
 Query Match 3.5%; Score 98; DB 7; Length 2668;
 Best Local Similarity 20.8%; Pred. No. 15;
 Matches 80; Conservative 67; Mismatches 105; Indels 132; Gaps 19;
 QY 49 KEQKGLNENALIRLIDEGCEVIOIKSPSGRTTKQBPMLPALAICSGCSDISTK 108
 DB 1017 KKQDLEAKNTQTLTADVKNBIIIEOQRKIFSLIOEKNELOQ--MLESV-----IAEK 1066
 QY 109 QAAFAVSEVCRIPHLTFPIQFKKDLKESM-----KCGMGRALRK--AIADWYN 157
 DB 1067 E-----OLKTDLKENIEMTIENOBELRLDDELKQOEIYAQEN 1106
 QY 158 ----EKGGWA-----LALAVTYKQ-----RNG 176
 DB 1107 HAIKKEGELSRCDLAEVEELKESQOLQKQOQLNVQEMSEMOKKINEIENLKNB 1166
 QY 177 WSHKDLRLSHLKPSEGLAIVTKYTKMKWEVHELKYKAL-----SVETEK--LKY 228
 DB 1167 LKNKE-LTLEHME--TERLELAQK-LNENYEEVKSITTKERKVLKELQSFETERDLRGY 1222
 QY 229 LEAVKRV-KRTQDELEVIHL-IEBHR-----LVREHLITNHLKSKVW 269
 DB 1223 IREIATGLOTEBELKIAHILKEHOETIDELRVSSEKTAQIINTQDLKSHTKQBEI 1282
 QY 270 KALLQEMPLTALLRNIGKMTANSVLEPGNSVSLVCEKLCNEKLLKARIRHFFHILALE 329
 DB 1283 PVLHEEQ---ELLPNVKEV---SETOETMNELELLTEOSTTKDSTTLARIEM----- 1328
 QY 330 TYKTGHGLRGKLMRPDEEILKAL 353
 DB 1329 -----ERLRINEKFOESQOEIKSL 1347
 RESULT 6
 US-10-453-372-1204
 ; Sequence 1204, Application US/10453372
 ; Publication No. US20060003323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alcobrook, et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
 ; FILE REFERENCE: 21402-589 A
 ; CURRENT APPLICATION NUMBER: US/10/453,372
 ; PRIOR FILING DATE: 2003-06-03
 ; PRIOR APPLICATION NUMBER: 09/789390
 ; PRIOR FILING DATE: 2001-02-23

```

; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CnarsSeqdist version 0.1
; SEQ ID NO 1204
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1204
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Query Match 3.4%; Score 95.5; DB 6; Length 600;

Best Local Similarity 18.8%; Pred. No. 2.9;

Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

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QY 95 ALAICSCSDISTQQAFAKAVSEV-----CRIPTHLFTFIOPK-----DL 135
DB 7 SVEICVNCSCVSENVLYNCEKVSYVRPNQKPEKMSFTHLNFQNNFNLITYPNTLNF 66
QY 136 KESNCKGCMGRALRKALADWYNEKGMAALAVTKYKQKNGWSHKDL-----LRLSHLKP 190
DB 67 SHAVALHGNKKQ-----NIEGAFGLSLKQHLANNELKILRADTFGLGIENLEY 119
QY 191 SSEGLAVTKYITGKMEVHELKYSVTEKLLKYLEAVEKVKTKDELEVIHLEE 250
DB 120 LQADYNLI-KYIERG--AFNKLHLKVL-IINDNLISPL-----P 155
QY 251 HRLVREHLTNHLKSKEVWKALLOEMPLTALLRLYLGKMTANSVLE--GENSEVSLVCEKLC 309
DB 156 DNIFRFASLT-HL---DIRGNRIQKLPYIGVLEHIGVLEQLQEDNPNWNSCDDLPLKAW 211
QY 310 NEKLKARLHPHILALETKYTGHLRGKLRKRPDEELIKALDAAFYKTFKTEVPTGK 369
DB 212 LENN-----PYNIVYGEAICETPSDLYGRLL-----LKETNK 242
QY 370 RFLAADVVSAMORVUG-----SILNASTYAAAMCMVYTRTEKDSYVVASDENVP 421
DB 243 QELCPMGTSDFVRIILPPSQLENGYYTPNGHTTQTSLHRLVYTRPKTYPNSKISG-IVA 301
QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETFAGVHPAI 481
DB 302 GKALSNRLSOIYVQTRVPP-LTPCPAPCC--KTH-PSDLGSLVNCQEKNIQSMSELI 357
QY 482 ALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDTGAL-----DVIR 531
DB 358 PKPLNAKKLHV-----NGNSIKDVDSDFDTBEGDLHLHLSNQITVTKGVFHH 406
QY 532 NPT 534
DB 407 NLT 409
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RESULT 7
US-10-453-372-1210
; Sequence 1210, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:

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; APPLICANT: Alisbroock, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CnarsSeqdist version 0.1
; SEQ ID NO 1210
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1210
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Query Match 3.4%; Score 95.5; DB 6; Length 819;

Best Local Similarity 18.8%; Pred. No. 4.6;

Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

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QY 95 ALAICSCSDISTQQAFAKAVSEV-----CRIPTHLFTFIOPK-----DL 135
DB 5 SVEICVNCSCVSENVLYNCEKVSYVRPNQKPEKMSFTHLNFQNNFNLITYPNTLNF 64
QY 136 KESNCKGCMGRALRKALADWYNEKGMAALAVTKYKQKNGWSHKDL-----LRLSHLKP 190
DB 65 SHAVALHGNKKQ-----NIEGAFGLSLKQHLANNELKILRADTFGLGIENLEY 117
QY 191 SSEGLAVTKYITGKMEVHELKYSVTEKLLKYLEAVEKVKTKDELEVIHLEE 250
DB 118 LQADYNLI-KYIERG--AFNKLHLKVL-IINDNLISPL-----P 153
QY 251 HRLVREHLTNHLKSKEVWKALLOEMPLTALLRLYLGKMTANSVLE--GENSEVSLVCEKLC 309
DB 154 DNIFRFASLT-HL---DIRGNRIQKLPYIGVLEHIGVLEQLQEDNPNWNSCDDLPLKAW 209
QY 310 NEKLKARLHPHILALETKYTGHLRGKLRKRPDEELIKALDAAFYKTFKTEVPTGK 369
DB 210 LENN-----PYNIVYGEAICETPSDLYGRLL-----LKETNK 240
QY 370 RFLAADVVSAMORVUG-----SILNASTYAAAMCMVYTRTEKDSYVVASDENVP 421
DB 241 QELCPMGTSDFVRIILPPSQLENGYYTPNGHTTQTSLHRLVYTRPKTYPNSKISG-IVA 299
QY 422 CPVTTDMTLQOVLMAMSOIPAGGTDGSLPMIWAOKTNPADVFIYFTDNETFAGVHPAI 481
DB 300 GKALSNRLSOIYVQTRVPP-LTPCPAPCC--KTH-PSDLGSLVNCQEKNIQSMSELI 355
QY 482 ALREYRKMDIPAKLIVCGMTSNGFTIADPDRGMLDMCGFDTGAL-----DVIR 531
DB 356 PKPLNAKKLHV-----NGNSIKDVDSDFDTBEGDLHLHLSNQITVTKGVFHH 404
QY 532 NPT 534
DB 405 NLT 407
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Db 357 GKALSNRNLISQIVSYQTRVPP-LTPCPAPFC--KTH-PSDLGLSVNCOEKNIQMSLELI 412
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPDDRGMLDMCGFDTGAL-----DYIR 531
Db 413 PKPLNAKGLHV-----NGNSIKDVDSDFTFEGDLHLHLSNOITVIKGVFH 461
QY 532 NPT 534
Db 462 NLT 464

RESULT 10
US-10-453-372-1208
; Sequence 1208, Application US/10453372
; Publication No. US2006003233A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqdist version 0.1
; SEQ ID NO 1208
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1208

Query Match 3.4%; Score 95.5; DB 6; Length 876;
Best Local Similarity 18.8%; Pred. No. 5;
Matches 91; Conservative 78; Mismatches 191; Indels 123; Gaps 20;

QY 95 ALAICSCSDISTKQAAFKAVSEV-----CRIFTHLFTFIQFK-----DL 135
Db 62 SVEICNVSCSVENVLYVNCERKVSVPYRNQKRPWNSFPHILANQNNTLILPTPLNF 121
QY 136 KESMKCGMGARLAKALADWTNEKGMALALAVTYKORNGSMHKL-----LRLSHKP 190
Db 122 SHAVSLHGNKQLQ-----NIEGAFILGSLAKQLHLNNNELKITLADTFGLIENLEY 174
QY 191 SSEGLATVTKITTKGKVEVHELYEKALSVETEKLLKLEAVEKVKRTKDELEVHILIE 250
Db 175 LQADVNLTKYIERG--AFNKLHLKVL--ILNDNLISPL-----P 210
QY 251 HRLVREHLTWNLKSKVEWKALLOEMPLTALLRLNGKMTANSVLE--PGNSEVSYCEKLC 309
Db 211 DNIRFASLT-HL--DIRGNRIQKLPYIGVLEHIGRVVEIQLEENPNWCSGDLIPLKAW 266
QY 310 NEKLKKARHPHILIALETVKTGHGRLKMKRPDEEILKALDAFYKTFKVEPTGK 369
Db 267 LENN-----PYNIVIGELCETPSDLYGRL-----LKETNK 297

QY 370 RFLAVDVASAMQORVLG-----SILNASTVAAMCVNTRTEKDSYVAFSDMEVP 421
Db 298 QELCPMGTSDFVRIILPESQLENGYTTTPNGHTTQISLHLVLPKPTTPSKISG-IVA 356
QY 422 CPVTTDMTLQOVLVAMNSQIPAGTDCSLPMIAOKTTPADVIFVFTDNETFAGVHPAI 481
Db 357 GKALSNRNLISQIVSYQTRVPP-LTPCPAPFC--KTH-PSDLGLSVNCOEKNIQMSLELI 412
QY 482 ALREYRKMDIPAKLIYCGMTSNGFTIADPDDRGMLDMCGFDTGAL-----DYIR 531
Db 413 PKPLNAKGLHV-----NGNSIKDVDSDFTFEGDLHLHLSNOITVIKGVFH 461
QY 532 NPT 534
Db 462 NLT 464

RESULT 11
US-10-878-556A-113
; Sequence 113, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; PRIOR FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ubp5_human
; DATABASE ENTRY DATE: 1996-02-01
US-10-878-556A-113

Query Match 3.4%; Score 95; DB 6; Length 858;
Best Local Similarity 20.0%; Pred. No. 5.3;
Matches 120; Conservative 85; Mismatches 217; Indels 178; Gaps 34;

QY 37 LCFSGEGGYIKQKGLENAEALI-----RLIEDRGCEVYIOIKSFQEGRTTKQ 90
Db 99 LAIGVEGG-EDLSSEKFELEDVQIVILPYLEIARGLG-----GLPDIYRDVTSAYE 152
QY 91 PMLPALAICSCSDISTKQAAFKAVSEVCRIPTHLFTFIQFKDLK-----ESMKCGMW 144
Db 153 ALISA-----DSASRKQEVQAWDGEVRQVSKAFSLKQLDNPARI.PPCGMKCSKCDM- 204
QY 145 GRALRKALADWTNEKGMALALAVTYKORNGSMHKLRLSHKPSSEGLATVTKYTK 204
Db 205 ---RENL--WLNLTDS--ILCGRYFDGSGNNH--AAEHYRETYPLAVKLGTTTP 253
QY 205 GWKEVHELYEKALSVETEKLLKYLE-----AVEKVKTKDELEVHILIEHRLVREH 257
Db 254 DGADVYS-YDEDDVLD-PSLAELHSHFGIDMLKMQTKDTMTLE-----IDMNGRIGE- 306
QY 258 LLTNHLKSKVEWKALQE--MPLTAL-----LRNLGKOT-ANSVLEPGNSEVSL--V 304
Db 307 -----WE-LIQSGVFLKPLFGPGYTGIRNGNSCYLNSVQVLRIPDPQRKY 354
QY 305 CEKLCNEKLKKARHP---PHILIALETYTGHLGAGLKKRPDEE----- 348
Db 355 VDKL--EKIPQNAFTDPTODFSQVLA---KLGGHLSGEYSKVPSPSGDERVPEQREV 408
QY 349 -----ILKALDAAPKTFKT-VEPTGKPLAV-----DVSASMNQORVLGSLNAST 394
Db 409 ODGIAPMKFALIKGHPFESTNRQDAQEFLLHIMMVENCSSEPNVFPFLVBEK 468
QY 395 VAAAMCVNVTREKDSYVAFSDMEVPCPVTTDMTLQOVL-----MA 436

Db 469 IKCLATEKVKYTORVDYIM-----QLPVMDALNKEELLEYEKKQAEKKALPELV 523
Qy 437 MSQIP-----AGTDCSLPMIW-----AQKTPA---DVFIPTNNEPAGVH 478
Db 524 RAQVPSSCLEAYGAPEDVDPMSTALQAKSVAVKTRFASFPPDLVYIQIKKTF----- 578
Qy 479 PALMREKRMODI-----PALYICGMTSNGF-----TIADPD-RCGLDMWC 521
Db 579 ---GLDWVPKLDVSIEMPEELDISQLKGTQLQPEEELPDIAPELVTPDEPKSLGFTYG 635

RESULT 12

US-10-467-657-3988
; Sequence 3988, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04
; SEQ ID NO 3988
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3988

Query Match 3.4%; Score 94; DB 6; Length 612;

Best Local Similarity 21.5%; Pred. No. 4;
Matches 69; Conservative 54; Mismatches 138; Indels 60; Gaps 11;

Qy 40 GSEGGTYIYKEQKLGLENALIRLIEDRGCEVIOEIKFSQSGRTTKQEPMLPALAIC 99
Db 148 GAKGCGNRKKGAKKQDYTSANKKARSQNGKAVQDKHTEENAKTDSDELKAAYAA 207
Qy 100 SQCSDISTKQAAFKAVSEVCAIPTHLPFTIQPKDKESMKCGMGRALKAIADWNEK 159
Db 208 T--NDEVNKKALLKQSEGMLHVSNSLKQLQGERIRQERIR---QERIRQA-----R 254
Qy 160 GMALALAVTKYKONGS-----HKDLRL-----SHLKSSSEGL 195
Db 255 GN-----LASVNRKQBEAMDKFQKLTETELNRLKTEVAATYAOISRFVSGNYKNSRPAVAL 310
Qy 196 AI-----VTKYITGKMK--VHELYK--EKALSVETEKLLKYLEAVEKVKRTD 240
Db 311 FKAABEPGQKRFRLKRYVANSNREVVQDLKQKALAVQEKINELARKLQIQAQV 370
Qy 241 ELEVIHLIEHRLVREHLITNHLKSKKVKALLQ---EMPTALLNIGKMTANSVLEPG 297
Db 371 SLKKQGVTDAAEQESRRQNAKISDAKRLQKNGEOQLNKLNLSEKKAHERIODA 430
Qy 298 NSESVLVEKL--CNELKLLKA 317
Db 431 EAKRKLAEAKLAAEKARKEA 451

RESULT 13

US-11-052-554A-130
; Sequence 130, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A

; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 130
; LENGTH: 1244
; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-11-052-554A-130

Query Match 3.4%; Score 94; DB 7; Length 1244;

Best Local Similarity 18.2%; Pred. No. 11;
Matches 129; Conservative 96; Mismatches 209; Indels 276; Gaps 35;

Qy 6 NQOMPLNEKOIANSODGVWQVTDNRLHRLFCGSEGGTYIYKEQKLGLENAE---AL 61
Db 513 NSYSPIKRIRVNRSTGVTV-----FGLDGGSYLLQDSTNKKSVSKQSLTL 558
Qy 62 IRLIEDRGCEVIOEIKFSQSGRTTKQEPMLPALAICQSCSDISTKQAAKAVSEVCI 121
Db 559 LTKSSGNSNKKVLDL-----DKOKQFL-----KPARQA-----KT 590
Qy 122 PTHLPFTIQPKDKESMKCGM-----GRALKAIADWNEKGMALALAVTKYK 172
Db 591 NTFYSTNPAFSPFPINETIK--SWPKHRELILANLVNASID--QOKKASKALTEAFNRYK 647
Qy 173 -----QRNGSHKDLRLSHLK-----PSSBGLAVTKYI 202
Db 648 ELIKFAPVALATTMISFYPPQMKALNNKLEBANLNQNNQANPTWINGLSAKLPYV 707
Qy 203 -TKG-----WKEVHELYKKAALSVETEKLLKYLEAVEKVKR----- 237
Db 708 NTNGVYEKLNNYFPLTKTLMPKVQ--BERTSISEBSNKKTKTADVDKIRDKILENIQ 765
Qy 238 -----TDEBLE-----VIHLIEHR-----LV 254
Db 766 TKVNDPVRKDKLPALAPPAVSNVILLVNDKVLSSGANSLSLQSDKVNPLSPML 825
Qy 255 REHLITNHL--KSKVWFKAL-----LOEMPLYT--ALLENIG-----KMTA 290
Db 826 KQAFPNNDLPFKAQQLKFDIOEKSSNNGMOSSTTNDADALSKYIGNVYTTAAKLTD 885
Qy 291 NSVLBPNGSE-----VSLVEKLCNEKLLK--KARIHPEHILIAETRYTGHLRGK 340
Db 886 KSIY--GNPKKKFELFRLANFEASIDKSFVNDKAVIDHYRFITYLQ----- 932
Qy 341 LKMRPDEELKALDAFYKTFKTEVEPTGRF--LAVDVSASNV--QRVLGSIINA 392
Db 933 --WLVDQKL-----KNFKSLKLTNMLKFEVAFIYKNTETNFSNPQVFSYFY 981
Qy 393 STVAANMCMVVRTRKDSVYVAFSDMBVCPYTMTLTQOVVAMASQIPAGTDCSLPMI 452
Db 982 ENSASBEVSESTQTLDPNNFFY-----KTTIKPTVO--AIQOV-----ASIALV 1022
Qy 453 WAQKTNTPADVFIPTDNETPAGVHPA-----IALREYKRMKDIPAKLIYVG 500
Db 1023 QKQCMQONSSTHYGTGLSTSSMFDASSRAIILQITKTSLOQYGSMDQ--KTIIG 1080
Qy 501 WTSNGFTIADPDRGMLDMCGFDYGA-----LDVIKNTFD 536
Db 1081 -TNNQILL-----DRIAVQLSGINPSTWNGSGKTIATYFQVDVAGNPTLD 1125

RESULT 14

US-10-878-556A-169
; Sequence 169, Application US/10878556A
; Publication No. US2005026399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.

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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:05:43 ; Search time 76 Seconds
(without alignments)
4994.398 Million cell updates/sec

Title: US-10-615-515-6
Perfect score: 2787
Sequence: 1 MBSVNMQPLNKRQANSQ.....MCGFDGALDVIRNFTLDMT 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2784	99.9	538	1 R060_HUMAN	P10155 homo sapien
2	2735	98.1	534	2 OSLJ99_HUMAN	Q51J99 homo sapien
3	2732	98.0	534	2 O86WL3_HUMAN	Q86WL3 homo sapien
4	2659	95.4	525	2 OSLJAO_HUMAN	Q51JAO homo sapien
5	2657	95.3	518	2 OSLJ98_HUMAN	Q51J98 homo sapien
6	2654	95.2	518	2 O86WL4_HUMAN	Q86WL4 homo sapien
7	2541	91.2	538	1 R060_MOUSE	Q08648 mus musculu
8	2535	91.0	538	2 O8R562_MOUSE	Q8R562 mus musculu
9	2532	90.9	538	2 O80WL2_MOUSE	Q80WL2 mus musculu
10	2532	90.9	547	2 OTT40_MOUSE	Q7T40 mus musculu
11	2269	81.4	538	1 R060_XENLA	P43700 xenopus lae
12	1544.5	55.4	547	2 Q4SP4_TITNG	Q4SP4 tetradon n
13	1517	54.4	558	2 Q5M7X5_BRARE	Q5M7X5 brachydano
14	1265	45.4	244	2 OSLJ97_HUMAN	Q51J97 homo sapien
15	1017.5	36.5	644	2 O61K10_CABBR	Q61K10 caenorhabdi
16	1011	36.3	1	1 R060_CABEL	Q27274 caenorhabdi
17	861	30.9	552	1 O852T5_9CUD	Q852T5 mycobacteri
18	798.5	28.7	531	1 R060_DEIRA	Q9T486 deinococcus
19	265.5	9.1	552	1 Q7UEC3_RHOBA	Q7UEC3 pseudomonas
20	255	9.1	514	2 Q4KEC3_PSEFP	Q4KEC3 pseudomonas
21	223	8.0	21	2 O8ZLH8_SALTY	Q8ZLH8 salmonella
22	205	7.4	517	2 O57IV5_SALCH	Q57IV5 salmonella
23	201	7.2	560	2 OSLMW2_STIRO	Q5LMW2 silicibacte
24	189.5	6.8	637	2 Q9W4R7_DROME	Q9W4R7 drosophila
25	180.5	6.5	719	1 T880_TETTH	Q94818 tetrathymena
26	165.5	5.9	1187	2 O6XJ03_MOUSE	Q6XJ03 mus musculu
27	143.5	5.1	712	2 O6ZU09_HUMAN	Q6ZU09 homo sapien
28	133.5	4.8	1937	2 O6SNT2_9PERO	Q6SNT2 silpserca c
29	132.5	4.8	786	2 O91520_THYTH	Q91520 thunnus thy
30	132	4.7	654	2 O6QUR8_GASAC	Q6QUR8 gasterosteus
31	132	4.7	1929	2 O98T06_9PERC	Q98T06 notothenia

ALIGNMENTS

RESULT 1	ALIGNMENTS
32 130.5 4.7 1936 2 Q90YF6_PARPO	Q90YF6 paracitrich
33 130.5 4.7 1937 1 MYH8_HUMAN	P13535 homo sapien
34 129.5 4.6 1938 1 MYSS_CHICK	P13538 gallus gall
35 129 4.6 975 2 Q98T05_9PERC	Q98T05 notothenia
36 128 4.6 799 2 Q4SZ8_TETNG	Q4SZ8 tetradon n
37 128 4.6 1938 2 Q8MJV0_HORSE	Q8MJV0 equus caball
38 127.5 4.6 1171 2 Q6DJR2_XENTR	Q6DJR2 xenopus tro
39 126 4.5 1938 2 Q91BD7_SERDU	Q91BD7 seriola dum
40 124.5 4.5 244 2 Q7PYC6_ANOGA	Q7PYC6 anopheles g
41 124.5 4.5 1935 1 MYSS_CYPCA	Q20339 cyprinus ca
42 124 4.4 766 2 O51EZ2_ENTHI	Q51EZ2 entamoeba h
43 124 4.4 1937 1 MYH8_MOUSE	P13542 mus musculu
44 123 4.4 1939 2 Q9TV61_PIG	Q9TV61 sus scrofa
45 123 4.4 3616 2 Q9W6V0_CHICK	Q9W6V0 gallus gall

RESULT 1	ALIGNMENTS
AC P10155; Q92787; Q9H1W6;	
DT 01-MAR-1989 (Rel. 10, Created)	
DT 25-OCT-2004 (Rel. 45, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE 60-kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa	
DE ribonucleoprotein Ro) (RoRNP) (Ro 60 kDa autoantigen) (TROVE domain	
DE family member 2) (Sjogren syndrome type A antigen) (SS-A) (Sjogren	
DE syndrome antigen A2).	
GN Name=TROVE2; Synonyms=RO60, SSA2;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RA MEDLINE=89071722; PubMed=320833;	
RT "Molecular analysis of the 60-kDa human Ro ribonucleoprotein.";	
RL Proc. Natl. Acad. Sci. U.S.A. 85:9479-9483(1988).	
RA MEDLINE=89198084; PubMed=2649513;	
RT "Isolation and characterization of a cDNA clone encoding the 60-kD	
RL component of the human SS-A/Ro ribonucleoprotein autoantigen.";	
RL J. Clin. Invest. 83:1284-1292(1989).	
RA NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM LONG).	
RP Buyon J.P., Didonato F., Tseng C.E., Raebbaum W., Morris A.,	
RA Hamel J.C., Chan B.K.L.;	
RT "Identification and characterization of an alternative mRNA transcript	
RL of the 60-kD SS-A/Ro ribonucleoprotein encoding the N-terminal RNA	
RL binding domain alone.";	
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.	
RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RP Human chromosome 1 international sequencing consortium;	
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
RA TISSUE=Testis;	
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,	
RA Hopfner R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stachleiko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,	
RA Bronstein M.J., Usdin T.B., Toshiyuki S., Carlini P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	

RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Nadeau A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skelton U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP INTERACTION WITH RIP1.
 RC TISSUE=Keratinocyte;
 RX MEDLINE=20015020; PubMed=10545525;
 RA Wang D., Buyon J.P., Zhu W., Chan E.K.L.,
 RT Defining a novel 75-kDa phosphoprotein associated with SS-A/Ro and
 RT identification of distinct human autoantibodies.";
 RL J. Clin. Invest. 104:1265-1275(1999).
 CC FUNCTION: RNA-binding protein that binds to several small
 CC cytoplasmic RNA molecules known as Y RNAs. May stabilize these
 CC RNAs from degradation.
 CC -Y- SUBUNIT: Binds RIP1.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=PI0155-1; Sequence=Displayed;
 CC Name=Short; Synonyms=60E2;
 CC IsoId=PI0155-2; Sequence=VSP_005911, VSP_005912;
 CC -I- DISEASE: Sera from patients with systemic lupus erythematosus
 CC (SLE) often contain antibodies that react with the normal cellular
 CC SSA2 protein as if this antigen was foreign.
 CC -I- SIMILARITY: Belongs to the Ro 60 kDa family.
 CC -I- SIMILARITY: Contains 1 TROVE domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J04137; AAA35493.1; -; mRNA.
 CC EMBL: M25077; AAA35532.1; -; mRNA.
 CC EMBL: M25077; AAA35532.1; -; mRNA.
 CC EMBL: U4388; AAB81553.1; -; Genomic DNA.
 CC EMBL: U4388; AAB81553.1; -; Genomic DNA.
 CC EMBL: AL136370; CAC17589.1; -; Genomic DNA.
 CC EMBL: BC036658; AA336558.1; -; mRNA.
 CC PIR: A31760; A31760.
 CC EMBL: ENSG00000116747; Homo sapiens.
 CC HGNC: HGNC:11313; TROVE2.
 CC MIM: 600063; -.
 CC MIM: 234700; -.
 CC GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 CC GO: GO:0003723; F:RNA binding; TAS.
 CC GO: GO:0006383; P:transcription from RNA polymerase III promoter; TAS.
 CC InterPro: IPR008858; TROVE.
 CC Pfam: PF05731; TROVE; 1.
 CC PROSITE: PS0988; TROVE; 1.
 CC Alternative splicing; Antigen; Ribonucleoprotein; RNA-binding;
 CC Systemic lupus erythematosus.
 CC TROVE.
 CC DOMAIN 16 369
 CC VARSPIC 195 205
 CC LAITKTYITNG -> KKKIFTKKKG (in isoform
 CC Short).
 CC /Frid=VSP_005911.
 CC Missing (in isoform Short).
 CC /Frid=VSP_005912.
 CC R -> K (in Ref. 1).
 CC GMLDMGFDVGGALDVINFTLDMT -> ALQNTLTKNSF
 CC (in Ref. 2).
 CC SEQUENCE 538 AA; 60671 MW; CD735B1DF2B13098 CRC64;

Query Match 99.9%; Score 2784; DB 1; Length 538;
 Best Local Similarity 99.8%; Pred. No. 3,4e-178;
 Matches 537; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEESVNOQPLNEKQIANSQDGVVQVDTMNRHRLFCGSEGGTYIKKQKLGLENAA 60
 DB 1 MEESVNOQPLNEKQIANSQDGVVQVDTMNRHRLFCGSEGGTYIKKQKLGLENAA 60
 QY 61 LRLIDGKGCCEYIOIKSPSOEGRTTKOEPMFALAISQCSIDITKQAFRAVSEVCR 120
 DB 61 LRLIDGKGCCEYIOIKSPSOEGRTTKOEPMFALAISQCSIDITKQAFRAVSEVCR 120
 QY 121 IPTHLETFIOFKKDLKESMKCGMGRALKAIADWYNEKGMALALAVTKYKQKNGSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMGRALKAIADWYNEKGMALALAVTKYKQKNGSHK 180
 QY 181 DLRLSHLKPSSEGLAVTKYITGKKEVHELYKERALSVETKLLKYLEAVEKVKRTKD 240
 DB 181 DLRLSHLKPSSEGLAVTKYITGKKEVHELYKERALSVETKLLKYLEAVEKVKRTKD 240
 QY 241 ELEVTILIEHRIVREHLLTNHLKSKKWKALLQEMPLTALLNLTGKMTANSTLBPQNSE 300
 DB 241 ELEVTILIEHRIVREHLLTNHLKSKKWKALLQEMPLTALLNLTGKMTANSTLBPQNSE 300
 QY 301 VSLVCEKLCNEKLLKKARLHPHILLALETTYTGHGRLGKLRPDEILKALDAAFYKT 360
 DB 301 VSLVCEKLCNEKLLKKARLHPHILLALETTYTGHGRLGKLRPDEILKALDAAFYKT 360
 QY 361 EKTVEPTGRFLIADVSAQNRVLGSLINASTVAAMCMTTRTRKDSYVAFSDENV 420
 DB 361 EKTVEPTGRFLIADVSAQNRVLGSLINASTVAAMCMTTRTRKDSYVAFSDENV 420
 QY 421 PCVTTDMTLQVLLAMMSQIPAGCTDCSLPMIAQKTNTPADVFYFTDNETFAGGVHPA 480
 DB 421 PCVTTDMTLQVLLAMMSQIPAGCTDCSLPMIAQKTNTPADVFYFTDNETFAGGVHPA 480
 QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMGFPDGLADVIRNFTLDMT 538
 DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMGFPDGLADVIRNFTLDMT 538
 RESULT 2
 Q5LJ99 HUMAN PRELIMINARY; PRT; 534 AA.
 ID Q5LJ99 HUMAN PRELIMINARY; PRT; 534 AA.
 AC Q5LJ99
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro).
 GN Name=SSA2; ORFName=RP11-101E13.3-005;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Whitehead S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AL136370; CA110823.1; -; Genomic DNA.
 DR GO: GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO: GO:0004618; F:phosphoglycerate kinase activity; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR GO: GO:0006096; P:glycolysis; IEA.
 DR InterPro: IPR001576; PGK.
 DR InterPro: IPR008858; TROVE.
 DR Pfam: PF05731; TROVE; 1.
 DR PROSITE: PS0988; TROVE; 1.
 DR Ribonucleoprotein; Viral nucleoprotein.
 KW Ribonucleoprotein; Viral nucleoprotein.
 SQ SEQUENCE 534 AA; 60169 MW; 785F949FED55344 CRC64;
 Query Match 98.1%; Score 2735; DB 2; Length 534;

Best Local Similarity 99.8%; Pred. No. 6,4e-175;
Matches 527; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
QY 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
QY 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
QY 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
DB 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
QY 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
DB 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
QY 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
DB 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
QY 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
QY 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
QY 361 PKTVEPTGKRFLLADV SASMNOVLGSIINASTVAAMCMVTRTEKDSYVAFSDEMV 420
DB 361 PKTVEPTGKRFLLADV SASMNOVLGSIINASTVAAMCMVTRTEKDSYVAFSDEMV 420
QY 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
DB 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
QY 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
DB 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528
DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528

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RESULT 3
ID 086WL3 HUMAN PRELIMINARY; PRT; 534 AA.

```

AC 086WL3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gastric cancer multi-drug resistance protein variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Han Q., Wang X., Shi Y., Ding J., Fan D.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY205315; AAC47002.1; -; mRNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR InterPro; IPR00858; TR0VE.
DR Pfam; PF05731; TR0VE.1.
DR PROSITE; PS50988; TR0VE.1.
SQ SEQUENCE 534 AA; 60197 MW; 63A4B96A77B6DD2D CRC64;

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Query Match 98.0%; Score 2732; DB 2; Length 534;
Best Local Similarity 99.6%; Pred. No. 1e-174;
Matches 526; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60

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QY 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
QY 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
DB 181 DLRLSHLKSSSEGLAVTKYITKGMEVHELYEKKALSVETELKYLEAVEKVKTRD 240
QY 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
DB 241 ELVYIHILIEBRLVREHLITNHLKSKVWKLLOEMPLTALLRLNGKMTANSVLEPGNSE 300
QY 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
DB 301 VSLVCEKLCNEKLLKKARIHFPFILIALETYKTGHGRGKLKWRPDEILKALDAAFYKT 360
QY 361 PKTVEPTGKRFLLADV SASMNOVLGSIINASTVAAMCMVTRTEKDSYVAFSDEMV 420
DB 361 PKTVEPTGKRFLLADV SASMNOVLGSIINASTVAAMCMVTRTEKDSYVAFSDEMV 420
QY 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
DB 421 PCPYTDMTLOOVVMAVSQIPAGGTDCLPMIWAOKNTTPADVFIPTDNETPAGGVHRA 480
QY 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528
DB 481 IALREYRKMDIPAKLIVCGMTSNGFTIADPDDRGMLDMCGFDTGALD 528

```

RESULT 4

ID 05LJAO HUMAN PRELIMINARY; PRT; 525 AA.

```

AC 05LJAO;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro).
OS Name=SSA2; ORFNames=RP11-101E13.3-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Whitehead S.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136370; CA110822.1; -; Genomic DNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR Ribonucleoprotein; Viral nucleoprotein.
SQ SEQUENCE 525 AA; 92408125E1038544 CRC64;

```

Query Match 95.4%; Score 2659; DB 2; Length 525;
Best Local Similarity 99.4%; Pred. No. 7.9e-170;
Matches 513; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
DB 1 MESSVNQOPINKEKQIANSODGYVQVTDNMRLHRLFLCGSEGGTYIYKEQKLGLENBA 60
QY 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
DB 61 LIRLIEDRGCEVIOEIKSFQSGRTTKOEBMFLALICQCSDSISTKQAAFAKAVSEVCR 120
QY 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180
DB 121 IPTHLFTFIQPKDKLKSMMKCGMGRALRAKAIADWYNEKGMALALAVTKYKQRNGWSHK 180

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QY	181	DLLRISHKPSSEGLAITYTKYITTKGKVEHLYEKALSVSTFKLKYIAEAEVKRYTQD	240
Db	181	DLRLSHLKPSSEGLAIVTKYITTKGKVEHLYEKALSVSTFKLKYIAEAEVKRYTQD	240
QY	241	ELEVHHLIEEHRIYVEHLLTNHLKKEVWKALLOEMPLTALLRNIGKMTANSVLEPGNSE	300
Db	241	ELEVHHLIEEHRIYVEHLLTNHLKKEVWKALLOEMPLTALLRNIGKMTANSVLEPGNSE	300
QY	301	VSIVCEKLCNEKLLKKARIIHPHILIALETTYTGGLRGKLRPDEILIKALDAAFYKT	360
Db	301	VSIVCEKLCNEKLLKKARIIHPHILIALETTYTGGLRGKLRPDEILIKALDAAFYKT	360
QY	361	FKTVEPTGRFLLAVDVASAMNQRYLGSILNASTYAAMAMVYTRTEKDSYVAFSEDMV	420
Db	361	FKTVEPTGRFLLAVDVASAMNQRYLGSILNASTYAAMAMVYTRTEKDSYVAFSEDMV	420
QY	421	PCPYTTDMTLQOVLAMSGIIPAGGIDCSIPMTWAOKTTPADVFIYFTDNEFPAGGVHQA	480
Db	421	PCPYTTDMTLQOVLAMSGIIPAGGIDCSIPMTWAOKTTPADVFIYFTDNEFPAGGVHQA	480
QY	481	IATREYRKMDIPAKLIVCGMTSNPTIADPDQRGM	516
Db	481	IATREYRKMDIPAKLIVCGMTSNPTIADPDQRGM	516

RESULT 5

ID	05LJ98_HUMAN	PRELIMINARY;	PRT;	518 AA.
AC	05LJ98;			
DT	01-FEB-2005 (TrEMBLrel. 29, Created)			
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)			
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)			
DE	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro).			
GN	Name=SSA2, ORFNames=RP11-101B13.3-003;			
OS	Homo sapiens (human).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NOTCLEOTIDE SEQUENCE.			
RA	Whitehead S.;			
RL	Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AL136370; CA110824.1; -; Genomic DNA.			
DR	GO; GO:0030529; C:ribonucleoprotein complex; IEA.			
DR	GO; GO:0004618; F:phosphoglycerate kinase activity; IEA.			
DR	GO; GO:0003723; F:RNA binding; IEA.			
DR	GO; GO:0006096; P:glycolysis; IEA.			
DR	InterPro; IPR001576; PGK.			
DR	InterPro; IPR008858; TROVE.			
DR	Pfam; PF05731; TROVE; 1.			
DR	PROSITE; PSS0988; TROVE; 1.			
DR	Ribonucleoprotein; Viral nucleoprotein.			
DR	SEQUENCE 518 AA; 58483 MW; D3C550ADBB2761B CRC64;			

Query Match	95.3%	Score 2657	DB 2	Length 518
Best Local Similarly	99.8%	Pred. No. 1.1e-169		
Matches 513; Conservative	1	Mismatches 0	Indels 0	Gaps 0

Qy	1	MEESYVNOQPLNEKCIANSQDGYVWOYDMMNLHRLCGSGGCTYYTIEQULGLENAA	60
Dy	1	MEESYVNOQPLNEKCIANSQDGYVWOYDMMNLHRLCGSGGCTYYTIEQULGLENAA	60
Qy	61	LIRLIEDRGCEVIOBIRKSFQEGRTTKOEPMLPALAISQCSDSISTKQAPFAVSEVCR	120
Dy	61	LIRLIEDRGCEVIOBIRKSFQEGRTTKOEPMLPALAISQCSDSISTKQAPFAVSEVCR	120
Qy	121	IPHTLFTTIOPEKDDIKESMKCGMMGALPKALADWYNEKGMALALAVTKYKORNSMSHK	180
Dy	121	IPHTLFTTIOPEKDDIKESMKCGMMGALPKALADWYNEKGMALALAVTKYKORNSMSHK	180

QY	161	DLRLSHKPSSEGLAIYKTYITGKMEVHEIYKKAISVETKKLKYLAEAKVKTBD	240
DB	181	DLRLSHKPSSEGLAIYKTYITGKMEVHEIYKKAISVETKKLKYLAEAKVKTBD	240
QY	241	ELEVIHLIEERLVAREHLLTYNHLKSKEVWKALLOEMPTLALRLNGKMTANSVLEBGNSE	300
DB	241	ELEVIHLIEERLVAREHLLTYNHLKSKEVWKALLOEMPTLALRLNGKMTANSVLEBGNSE	300
QY	301	VSIVCEKLCNKKELKKARIHPPHILIALETYKTHGRLKLMRPDEEILKALDAAFYKT	360
DB	301	VSIVCEKLCNKKELKKARIHPPHILIALETYKTHGRLKLMRPDEEILKALDAAFYKT	360
QY	361	FKTVEPTGKRFLLAVDVSASMNQVRLSITLNASTYAAAMCMVVTREKOSYVAFSDEVY	420
DB	361	FKTVEPTGKRFLLAVDVSASMNQVRLSITLNASTYAAAMCMVVTREKOSYVAFSDEVY	420
QY	421	PCPVTITMTLQOVTLMANSQIPAGGVDGSLPMIWAQKTPADVFIYFTDNETFPAGGVHRA	480
DB	421	PCPVTITMTLQOVTLMANSQIPAGGVDGSLPMIWAQKTPADVFIYFTDNETFPAGGVHRA	480
QY	481	IALREYRKQMDIPAKLIVCGMTNSGFTIADPDR	514
DB	481	IALREYRKQMDIPAKLIVCGMTNSGFTIADPDR	514

RESULT 6

ID	O66W14	HUMAN		
AC	O66W14_1	HUMAN	PRELIMINARY;	PRT; 518 AA.
DT	01-JUN-2003	(TrEMBLrel. 24,		
DT	01-JUN-2003	(TrEMBLrel. 24,		
DT	01-MAR-2004	(TrEMBLrel. 26,		
DE	Gastric cancer multi-drug resistance protein variant.			
OS	homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Cetiartnhi; Homnidnae;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Han Q., Wang X., Shi Y., Ding J., Fan D.;			
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY205319; AAC47001.1; -, mRNA.			
DR	GO; GO:0030529; C:ribonucleoprotein complex; IEA.			
DR	GO; GO:0003723; C:rRNA binding; IEA.			
DR	InterPro; IPR008858; TROVE.			
DR	Pfam; PF05731; TROVE; 1.			
DR	PROSITE; PSS0988; TROVE; 1.			
SQ	SEQUENCE 518 AA; 5851 MW; 42C350BD263865A1 CRC64;			

Query Match	95.2%	Score 2654;	DB 2;	Length 518;
Best Local Similarity	99.6%	Pred. 0.17e-16;		
Matches 512; Conservative	2;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MEESYUNQOPIENKQIANSODGYVWQVTDNMRHHPFLCQSGSGGYIYIEOKJGLGENAE	60
Db	1	MEESYUNQOPIENKQIANSODGYVWQVTDNMRHHPFLCQSGSGGYIYIEOKJGLGENAE	60
QY	61	LIRLIEDRGCEVIOEIKSFSGEGRITTOEPMLFALATICSQSDISTKQAAFAVSEVCR	120
Db	61	LIRLIEDRGCEVIOEIKSFSGEGRITTOEPMLFALATICSQSDISTKQAAFAVSEVCR	120
QY	121	IPTHLFTTIQKRDUKESMKCGMMRRLARKALADYNYNEGGMALALATKYQYQORNMSHK	180
Db	121	IPTHLFTTIQKRDUKESMKCGMMRRLARKALADYNYNEGGMALALATKYQYQORNMSHK	180
QY	181	DLRLSHLKPSSSEGAIATVKYITTKQWKEVHELVEKSKALSVETEKLIKYLEAAVEKVKRTQD	240
Db	181	DLRLSHLKPSSSEGAIATVKYITTKQWKEVHELVEKSKALSVETEKLIKYLEAAVEKVKRTQD	240
QY	241	ELEVHILIEEHLVREHLLTNHLKSKEYWALKLOEMPJTALLRNIGKMTANSVLEPGNSE	300
Db	241	ELEVHILIEEHLVREHLLTNHLKSKEYWALKLOEMPJTALLRNIGKMTANSVLEPGNSE	300

RA Kannejell C.C., Fu S.M.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L81154; ALU7518.1; -, mRNA.
 DR MGI; MGI:106652; Ssa2.
 DR GO; GO:0030529; Cribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 KW Ribonucleoprotein.
 SQ SEQUENCE 538 AA; 60153 MW; 65B46C843FA4572E CRC64;
 Query Match 91.0%; Score 2535; DB 2; Length 538;
 Best Local Similarity 89.8%; Pred. No. 1,7e-161;
 Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;

QY 1 MESSVQNMQPLNEKQIANSODGYVQVDTMNRHLRFICFSGSEGTYIYKEQKLGLENAA 60
 DB 1 MEGSANQLOPLSEYQVNSGGCVQVDTMNRRLRFLCFSGSEGTYIYKEQKLGLENAA 60
 QY 61 LRLIEDGCGCEVIOIKFSQSGRTTKOBPMFLALATSCQSDISTKQAFKAVSEVCR 120
 DB 61 LRLIEDGCGCEVIOIKFSQSGRTAKOBPLFLALAVCSQCADINTKQAFKAVSEVCR 120
 QY 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 QY 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 QY 181 DLRLSHLKPSSSGALAVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 DB 181 DLRLSHLKPSSSGALAVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 QY 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLRNIGKMTANSVLEBGNSE 300
 DB 241 ELEVTHLIEBHQLVREHLLTNHLKSKVWKALLOEMPLTALLRNIGKMTANSVLEBGNSE 300
 QY 301 VSLVCEKLCNEKLLKAKRIHPHILIALETKYTGHLRGKLRPDEELIKALDAAFYKT 360
 DB 301 VSLICEKLSNEKLLKAKRIHPHVLIALETRYAGHGRGLKMIIPKDLQALDAAFYTT 360
 QY 361 FKTVEPTGKRFLLADVVSASMNQRLVLSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 DB 361 FKTVEPTGKRFLLADVVSASMNQRLVLSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 QY 421 PCVTTDTMTLQOVLTAAMSOIPAGTDCSLPMIWAOKTNTPADVFYITDNETFAGGVHRA 480
 DB 421 PEPVTTDTMTLQOVLTAAMNKVPAGNTDCSLPMIWAOKTNTPADVFVFTDNETFAGGVHRA 480
 QY 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDRGMLDMCGFDTGALDVIKNTFLDMI 538
 DB 481 VALREYRKMDIPAKLIIVCGMTSNGFTIADPDRGMLDMCGFDTGALDVIKNTFLDVI 538

RESULT 9
 ID 080M12 MOUSE PRELIMINARY; PRT; 538 AA.
 AC 080M12-
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE 60KD Ro/SSA autocantigen.
 GN Name=Ssa2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse S.J.M., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.U., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051974; AAH51974.1; -, mRNA.
 DR MGI; MGI:106652; Ssa2.
 DR GO; GO:0030529; Cribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR008858; TROVE.
 DR Pfam; PF05731; TROVE; 1.
 DR PROSITE; PS50988; TROVE; 1.
 SQ SEQUENCE 538 AA; 60171 MW; 7850C6E41C726BDA CRC64;

Query Match 90.9%; Score 2532; DB 2; Length 538;
 Best Local Similarity 89.8%; Pred. No. 2.7e-161;

Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;

QY 1 MESSVQNMQPLNEKQIANSODGYVQVDTMNRHLRFICFSGSEGTYIYKEQKLGLENAA 60
 DB 1 MEGSANQLOPLSEYQVNSGGCVQVDTMNRRLRFLCFSGSEGTYIYKEQKLGLENAA 60
 QY 61 LRLIEDGCGCEVIOIKFSQSGRTTKOBPMFLALATSCQSDISTKQAFKAVSEVCR 120
 DB 61 LRLIEDGCGCEVIOIKFSQSGRTAKOBPLFLALAVCSQCADINTKQAFKAVSEVCR 120
 QY 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 QY 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 DB 121 IPTHLETFIOFKKDLKESMKCGMMGRALKAKIADWYNEKGMALALAVTKYKQRNGMSHK 180
 QY 181 DLRLSHLKPSSSGALAVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 DB 181 DLRLSHLKPSSSGALAVTKYITKGWKEVHELYEKALSVETEKLYLEAVEKVKRTKD 240
 QY 241 ELEVTHLIEBHRLVREHLLTNHLKSKVWKALLOEMPLTALLRNIGKMTANSVLEBGNSE 300
 DB 241 ELEVTHLIEBHQLVREHLLTNHLKSKVWKALLOEMPLTALLRNIGKMTANSVLEBGNSE 300
 QY 301 VSLVCEKLCNEKLLKAKRIHPHILIALETKYTGHLRGKLRPDEELIKALDAAFYKT 360
 DB 301 VSLICEKLSNEKLLKAKRIHPHVLIALETRYAGHGRGLKMIIPKDLQALDAAFYTT 360
 QY 361 FKTVEPTGKRFLLADVVSASMNQRLVLSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 DB 361 FKTVEPTGKRFLLADVVSASMNQRLVLSIINASTVAAAMCMVTRTEKSSVVAFAFCDW 420
 QY 421 PCVTTDTMTLQOVLTAAMSOIPAGTDCSLPMIWAOKTNTPADVFYITDNETFAGGVHRA 480
 DB 421 PEPVTTDTMTLQOVLTAAMNKVPAGNTDCSLPMIWAOKTNTPADVFVFTDNETFAGGVHRA 480
 QY 481 IALREYRKMDIPAKLIIVCGMTSNGFTIADPDRGMLDMCGFDTGALDVIKNTFLDMI 538
 DB 481 VALREYRKMDIPAKLIIVCGMTSNGFTIADPDRGMLDMCGFDTGALDVIKNTFLDVI 538


```
RESULT 10
Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
ID Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
AC Q7TT40_MOUSE PRELIMINARY; PRT; 547 AA.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sna2 protein (Fragment).
Name=Sna2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helet F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomihyuki S., Carninci P., Prange C.,
RA Rha S.S., Loughlan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Boulford G.G.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko U., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywnicki M.I., Skalek U., Smallie D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Strausberg R.,
RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC052380; AAH52380.1; -; mRNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR008658; TROVE.
DR PROSITE; PS50988; TROVE; 1.
FT NON TER
SQ SEQUENCE 547 AA; 61272 MW; 2CF235A0C803510F CRC64;

Query Match 90.9%; Score 2532; DB 2; Length 547;
Best Local Similarity 89.8%; Pred. No. 2.7e-151;
Matches 483; Conservative 29; Mismatches 26; Indels 0; Gaps 0;
```

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Db 250 DLEVIHLIEBHQVLRHLLTNHLKSKYWKALLQEMPTALLRNIGKMTANSVLEPGNSE 309
Qy 301 VSLVCEKLNCKELKKARLHPHLLALATYTKGHGRLGKTKRPDEILKALDAAPFYKT 360
Db 310 VSLICEKLSNEKLLKKARLHPHLLALATYTKGHGRLGKTKRPDXLIQALDAAPFYTT 369
Qy 361 FKTVEPTGRKFLAVDSANORVLGSLINASTVAAACMVYTRTEKDSYVAFSDENV 420
Db 370 FKTVEPTGRKFLAVDSANORVLGSLINASTVAAACMVYTRTEKDSYVAFSDENV 429
Qy 421 PCFVTTDMTLQVLTAMMSQIPAGTDCSLPMIWAQKNTPADVFVFTDNETPAGVHPA 480
Db 430 PFPVTTDMTLQVLTAMMSQIPAGTDCSLPMIWAQKNTPADVFVFTDNETPAGVHPA 489
Qy 481 IALREYRKAMDIAKILVCGMTSGFTIADPPDRGRLDMCGPRTGALDVIRNFTLMDI 538
Db 490 VALREYRKAMDIAKILVCGMTSGFTIADPPDRGRLDMCGPRTGALDVIRNFTLMDI 547

RESULT 11
Ro60_XENLA STANDARD; PRT; 538 AA.
ID Ro60_XENLA STANDARD; PRT; 538 AA.
AC P42700;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 60-kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa
DE ribonucleoprotein Ro) (RoRNP) (TROVE domain family member 2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo, and Ovary;
RX MEDLINE=93348251; PubMed=7688474;
RA O'Brien C.A., Margelot K., Wolin S.L.;
RT "Xenopus Ro ribonucleoproteins: members of an evolutionarily conserved
RT class of cytoplasmic ribonucleoproteins."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7250-7254(1993).
CC -1- FUNCTION: RNA-binding protein that binds to several small
CC cytoplasmic RNA molecules known as Y RNAs. May stabilize these
CC RNAs from degradation.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the Ro 60 kDa family.
CC -1- SIMILARITY: Contains 1 TROVE domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; L15430; AAC38001.1; -; mRNA.
DR PIR; I51560; I51560.
DR InterPro; IPR008858; TROVE.
DR Pfam; PF05731; TROVE; 1.
DR PROSITE; PS50988; TROVE; 1.
KW Ribonucleoprotein; RNA-binding.
FT DOMAIN 16 369 TROVE.
SQ SEQUENCE 538 AA; 60688 MW; 548C17B0A9EBBFD6 CRC64;

Query Match 81.4%; Score 2269; DB 1; Length 538;
Best Local Similarity 78.6%; Pred. No. 1.2e-143;
Matches 423; Conservative 59; Mismatches 56; Indels 0; Gaps 0;
```

DB 61 LRLRLDGGKCEVVOEIKTPSGEGRABKOEPTLFALAVCSQCSIDIKTKQAAPRAVPEVCR 120
QY 121 IPRHLFTFIQPKDKLKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 180
DB 122 IPRHLFTFIQPKDKLKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 180
QY 181 DLLRLRLHKLKSSGLAVTKYTKGWKEVHLYEKALSVETEKLLKYLEAVEKVKRTKD 240
DB 181 DLLRLRLHKLKSSGLAVTKYTKGWKEVHLYEKALSVETEKLLKYLEAVEKVKRTKD 240
DB 181 DLLRLRLHKLKSSGLAVTKYTKGWKEVHLYEKALSVETEKLLKYLEAVEKVKRTKD 240
QY 241 ELEVIHLIEEHLVREHLLTNHLKSKVWYKALLOEMPTALLRNLGKMTANSVLEPGNS 300
DB 241 ELEVIHLIEEHLVREHLLTNHLKSKVWYKALLOEMPTALLRNLGKMTANSVLEPGNS 300
QY 301 VSIIVCEKLCNEKLLKARIRHPHILALETKYKTHGKRGKLRPRDEILKALDAAPYKT 360
DB 301 VSIIVCEKLCNEKLLKARIRHPHILALETKYKTHGKRGKLRPRDEILKALDAAPYKT 360
QY 361 PKTVEPTGRFLLAVVSAVSMNORVLSIINASTVAAMCVVTRTEKDSYVAFSGDEMY 420
DB 361 PKTVEPTGRFLLAVVSAVSMNORVLSIINASTVAAMCVVTRTEKDSYVAFSGDEMY 420
QY 421 PCFVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNEPAGGVHRA 480
DB 421 PCFVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNEPAGGVHRA 480
QY 481 IALREPRKMDIPAKLIVCGMTSNGFTIADPPDRGMIDMGCFPTGALDVIRNTLDMI 538
DB 481 IALREPRKMDIPAKLIVCGMTSNGFTIADPPDRGMIDMGCFPTGALDVIRNTLDMI 538
QY 538 TALKQYREKKGIPAKLIVCMTSNGFTIADPPDRGMIDMGCFPTGALDVIRNTLDMI 538
DB 538 TALKQYREKKGIPAKLIVCMTSNGFTIADPPDRGMIDMGCFPTGALDVIRNTLDMI 538

RESULT 12
Q4SP44.TEIMG
ID Q4SP44.TEIMG PRELIMINARY; PRT; 547 AA.
AC Q4SP44.TEIMG
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
CHROMOSOME 15 SCAR14542, whole genome shotgun sequence.
GN ORFNames=GSTENG00014938001;
OC Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
Maucell E., Bouneau L., Fischer C., Ozouf-Coenaz C., Bernot A.,
Nicard S., Jaffe D., Fisher S., Luitalla G., Dobat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemond C., Skalli Z., Caticolico L., Poulin J., De Berardinis V.,
Cruaud C., Duprat S., Broclet P., Couanceau J.P., Gouzy J.,
Barra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RA Nature 431:946-957(2004).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RU Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAE01014542; CAP97528.1; -; Genomic DNA.
DR EMBL; CAE01014542; CAP97528.1; -; Genomic DNA.
SQ SEQUENCE 547 AA; 60290 MW; ED022BD11A3E727A CRC64;

Query Match 55.4%; Score 1544.5; DB 2; Length 547;
Best Local Similarity 53.0%; Pred. No. 4.6e-95;
Matches 290; Conservative 109; Mismatches 139; Indels 9; Gaps 4;
QY 1 MEESYNQOMPLNEKOTANSQDGYVQVDTMNLRLHFLCFSBGCTYYIEOK-LGLENA 59
DB 1 MEESYNQOMPLNEKOTANSQDGYVQVDTMNLRLHFLCFSBGCTYYIEOK-LGLENA 59
QY 60 ALIRLEDRGCEVVOEIKTPSGEGRABKOEPTLFALAVCSQCSIDIKTKQAAPRAVPEVCR 119
DB 60 ALIRLEDRGCEVVOEIKTPSGEGRABKOEPTLFALAVCSQCSIDIKTKQAAPRAVPEVCR 119
QY 120 RIPTHLFTFIQPKDKLKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 179
DB 120 RIPTHLFTFIQPKDKLKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 179
QY 121 RPPAQLFAFIQKKELKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 180
DB 121 RPPAQLFAFIQKKELKEKMGCGMGRALRAKADVYNEKCGMALALAVTKYKQRNMGSHK 180
QY 180 KDILRLSHKLKSSGLAVTKYTKGWKEVHLYEKALSVETEKLLKYLEAVEKVKRTK 239
DB 180 KDILRLSHKLKSSGLAVTKYTKGWKEVHLYEKALSVETEKLLKYLEAVEKVKRTK 239
QY 240 DELEVIHLIEEHLVREHLLTNHLKSKVWYKALLOEMPTALLRNLGKMTANSVLEPGNS 299
DB 240 DELEVIHLIEEHLVREHLLTNHLKSKVWYKALLOEMPTALLRNLGKMTANSVLEPGNS 299
QY 241 PCFVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNEPAGGVHRA 300
DB 241 PCFVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNEPAGGVHRA 300
QY 300 EVSLVCEKLCNEKLLKARIRHPHILALETKYKTHGKRGKLRPRDEILKALDAAPYKT 360
DB 300 EVSLVCEKLCNEKLLKARIRHPHILALETKYKTHGKRGKLRPRDEILKALDAAPYKT 360
QY 361 PKTVEPTGRFLLAVVSAVSMNORVLSIINASTVAAMCVVTRTEKDSYVAFSGDEMY 420
DB 361 PKTVEPTGRFLLAVVSAVSMNORVLSIINASTVAAMCVVTRTEKDSYVAFSGDEMY 420
QY 413 VAFSD-EMVPCVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNE 471
DB 413 VAFSD-EMVPCVTTDMTLQOVLAMASQIPAGTDCSLPIMVAKNTPEADVIFVETDNE 471
QY 421 LAYSGTVVPCAVTADMTALVAVTSVLSVPGTISTALIAAIAAMFVETEDTEV 480
DB 421 LAYSGTVVPCAVTADMTALVAVTSVLSVPGTISTALIAAIAAMFVETEDTEV 480
QY 472 FAGGVHRAIPALREYKMKMDIPAKLIVCGMTSNGFTIADPPDRGMIDMGCFPTGALDVIR 531
DB 472 FAGGVHRAIPALREYKMKMDIPAKLIVCGMTSNGFTIADPPDRGMIDMGCFPTGALDVIR 531
QY 531 LMFPSAPAFETIQKRRKTKGASKLVICLTNSGSLADTEBDGSLIGCFDGLSVIR 540
DB 531 LMFPSAPAFETIQKRRKTKGASKLVICLTNSGSLADTEBDGSLIGCFDGLSVIR 540

RESULT 13
Q5M7X5.BRARE
ID Q5M7X5.BRARE PRELIMINARY; PRT; 558 AA.
AC Q5M7X5.BRARE
DT 01-FEB-2005 (TEMBLrel. 29, Created)
DT 01-FEB-2005 (TEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Hypothetical protein (Fragment).
OS Bacteroides fragilis (Bacteroides) (Bacteroides).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Straussberg R.L., Feingold E.A., Grusec L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin J.M., Hong L.,
Shapletton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
Brownstein M.J., Uedlin T.B., Toehlyuk S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
Bosak S.A., McKernan K.J., Malek U.A., Gunaratne P.H.,
Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodighiero Y.S.N., Krzyzanski M.I., Skalek U., Smallie D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE-whole.
RA Director MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088391; AAH8391.1; -, mRNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR008858; TROVE.
DR Pfam; PF05731; TROVE; 1.
DR PROSITE; PS50988; TROVE; 1.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 558 AA; 61579 MW; 92158A20E24068E6 CRC64;

Query Match 54.4%; Score 1517; DB 2; Length 558;
Best Local Similarity 54.5%; Pred. No. 3.3e-93;
Matches 290; Conservative 99; Mismatches 135; Indels 8; Gaps 5;

QY 7 OMQPLNKQIANSDDGYVQVTDNNRLHRLFCPSGEGTYYIKKQKGLNVAALIRLIE 66
DB 33 QLSVANE-QVANSADR---SVTAAVCLRRFLCYSESSTYTKCPGLGIALSLIMQIE 88
QY 67 DGRCEVYIOEIKFSQSGRTTKQBPMLFALAICSCQSDISTKQAFKAVSEVCRIPHLF 126
DB 89 GGRSEVVDVBRNRNLGSAVRPNPGLFTLAVCSQHADCKTRQALRALKELCSPPQLF 148
QY 127 TFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHQDLRLS 186
DB 149 TPVQYKKEIKEG--SGMWGRALRRVVDVWGODGISLAQAVTCKKRAKSHQDLRLS 206
QY 187 HIKSSSGSLIVTKYTKGKWEVHELYEKALSVTEKLLKYLEAVEKVKTKQLEVIYI 246
DB 207 HMKRANNDIALVCKYITKGMGEBAVAEKSDQLQVPAYLBAVEKVKSTDEQELIH 266
QY 247 LIEBRLVREHLITNHLKSKVKALIQEMPTALLRNIGMTANSVLEPNSSEVLVCE 306
DB 267 LIEBRLVREHLITNHLKSKVKALIQEMPTALLRNIGMTANSVLEPNSSEVLVCE 306
QY 307 KLCNEKLKARIRHPHILALETYTGSGIRGLKRRPDEBILKALDAAYTKPYEVP 366
DB 327 RIQETVYLKAKTQPFNIIAASENVKRGHGRSKLKWEPDLDVQALDCAKCSISTEA 386
QY 367 TGRKFLAVNDVSAAMNQVIVGSIINASTVAAMCMVVRTRKDSVVAFSD-EMVPCPYT 425
DB 387 TGRKFLAVNDVSAAMNQVIVGSIINASTVAAMCMVVRTRKDSVVAFSD-EMVPCPYT 425
QY 426 TDMTIGQVILAMSGQIPAGTDCSLPMIAQKNTPADVFIPTDNRTFAGVHPALALRE 485
DB 447 SDMTLMQVAGLIIQTGGSTDCSLPITVASENEKTVDVFIILTNQGT-GENRPNDLTKM 505
QY 486 YRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMGCFPTGALDIVIRNFTLDM 537
DB 506 YRKQNDIPAKLIVCGMTSNGFTIADPDDRGMLDMGCFPTGALDIVIRNFTLDM 537

RESULT 14
Q5LJ97 HUMAN PRELIMINARY; PRT; 244 AA.
Q5LJ97 HUMAN PRELIMINARY; PRT; 244 AA.
AC 05LJ97
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Sjogren eyndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-

DE A/Ro) (Fragment).
GN Name=SSA2; ORFNames=RP11-101E13.3-004;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136370; CA110825.1; -, Genomic DNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR008858; TROVE.
DR Pfam; PF05731; TROVE; 1.
DR PROSITE; PS50988; TROVE; 1.
KM Ribonucleoprotein; Viral nucleoprotein.
FT NON TER 244
SQ SEQUENCE 244 AA; 28035 MW; 92C174AFE01E93B1 CRC64;

Query Match 45.4%; Score 1265; DB 2; Length 244;
Best Local Similarity 99.6%; Pred. No. 9e-77;
Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSVNMQPLNEKQIANSDDGYVQVTDNNRLHRLFCPSGEGTYYIKKQKGLNVAALIRLIE 60
DB 1 MESSVNMQPLNEKQIANSDDGYVQVTDNNRLHRLFCPSGEGTYYIKKQKGLNVAALIRLIE 60
QY 61 LIRLIEBGRCEVYIOEIKFSQSGRTTKQBPMLFALAICSCQSDISTKQAFKAVSEVCR 120
DB 61 LIRLIEBGRCEVYIOEIKFSQSGRTTKQBPMLFALAICSCQSDISTKQAFKAVSEVCR 120
QY 121 IPTHLPFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHQDLRLS 180
DB 121 IPTHLPFIQPKDKESMKCGMGRALRKALADWYNEKGMALALAVTKYKQNGSHQDLRLS 180
QY 181 DLRLSHLKSSEGLAVTKYTKGKWEVHELYEKALSVTEKLLKYLEAVEKVKTKQLEVIYI 240
DB 181 DLRLSHLKSSEGLAVTKYTKGKWEVHELYEKALSVTEKLLKYLEAVEKVKTKQLEVIYI 240
QY 241 ELKV 244
DB 241 ELKV 244

RESULT 15
Q6IK10 CABBR PRELIMINARY; PRT; 644 AA.
Q6IK10 CABBR PRELIMINARY; PRT; 644 AA.
AC Q6IK10
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein CBG09566.
GN Name=CBG09566;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
OC Rhabditidae; Peloderidae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01000044; CA86475.1; -, Genomic DNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR008858; TROVE.
DR Pfam; PF05731; TROVE; 1.
DR PROSITE; PS50988; TROVE; 1.
KM Hypothetical protein.

SEQ SEQUENCE 644 AA; 72850 MW; AB7EB0E0D7DEE5 CRC64;
Query Match 36.5%; Score 1017.5; DB 2; Length 644;
Best Local Similarity 36.7%; Pred. No. 1,3e-59;
Matches 216; Conservative 108; Mismatches 201; Indels 63; Gaps 8;
7 OMQPLNEKQJANSGDGVVQVMDNMRHLRPLCFGSEGGTYIYKEQKLGLENALIRLIE 66
DB QMEQVEGQVMENAGGFVFPVSDETQVRRLIIGSDKGYHQAENKILTIDNAQRIYIEIIQ 113
67 DGRGCEVIOEIKPSQSGRTTKQEPMLFALAICQCSDISTQ----- 109
DB KKGKHVYLHFLALINENRNPKNNSMLFLAICARVSTHDTTKNECPILHTYSEYIRAL 173
QY 110 --AAPFAVSEVCGRIPTHLFTPTQFKDKLKSMSKG-----MGRALRKALADYNKEGG 161
DB 174 HAAALRLPLPVCRTPTLTFEFVYCCQTIASSTAGAKSSTGWRSLRNAIIRKYEKTA 233
QY 162 MALALAVTKYKORNGMSHKDLRLSHLKPSSBGL-----AIVTKYITKG----- 205
DB 234 EKLAMLITKTPQREGSHRDLFRLAHENLMDGTHHTDRDLEREOLEFPAVKGLVKA 293
QY 206 -----MKVEHLYKEKALSV-----ETEKLLKYLEAVEKVKRTKDELEVIHL 247
DB 294 KKKANDEEKAKIESMDKRALKVPTTEQLVKEKSRALDLVEAYLSLKQEQSEVIVEA 353
QY 248 IEERHLYREHLTNHLKSKEVWKALLO-EMPLTALLNLGRMTANSVLEPGNSEVSLVCE 306
DB 354 IKKGGLVREHLPTSSLSLSKLVMETLFDVPMPTAMIRNLGKMTLVGALD--DNRVKSIVS 411
QY 307 KLGNKLLKKARITHPHILIALETVKTGHGLRGKLKWRPDEBILKALDAAFYTKPTVER 366
DB 412 RLTDQELRRARLHPLTLTARSYVARGQDKSGLTWEPNQKICDALLAGFYKAFVNSPP 471
QY 367 TGRKFLAVDVSAAMNQVLSILINASTVAAAMCMVVTREKDSYVAFSDEWVPCPVTT 426
DB 472 TGRKYCALALVSGMSGFVSSPLSCREAAATGMSLINLHNEAEVKVAFCDKLTLELPTK 531
QY 427 DMTLQOVLAMSGIIPAGCTCCSLPMIAQKTNTPADVIFVFTDNETPAGVHPALALREY 486
DB 532 DMKIGQVNDVNNLSFGSTDCGLPMTWATENNLLKFDVFIITDNDTWAGEIHPEAIKKY 591
QY 487 RKQMDI-PAKLIVCGMSTNGFTIADPDDRGMLDMWCGFDTGALDVIRNF 533
DB 592 REASGIDHAKVIVAMQAVNYSTADPSDAGMLDTTGFDSAVPOIVHEF 639

Search completed: January 13, 2006, 11:10:41
Job time : 78 secs